, Wed Mar 31 11:36:26 2004

Aae02361 Human tum
Abg70870 Human tum
Abr56556 Human can
Abu56653 Lung canc
Ade27781 Human pro
Abr58557 Human can
Abr58557 Human can
Aay00893 Human can
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Aay013381 Animan can
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Adc78533 Human PRO
Aabe0249 Human PRO
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Aabu89057 Human PRO
Abu71627 Human PRO
Abu71627 Human PRO
Abu8716616 Human Roc
Abr66150 Human sec

Jos on

26 262 14.0 277 4 AAB02361 Abg70870 Abg70870 Human tum 27 262 14.0 277 5 ABG70870 Abg70870 Abg70870 Human tum 29 262 14.0 277 6 ABS856 Abb26653 Abu56653 Lum canc 31 244 13.1 277 6 ABE85657 Abu5665781 Abu5665781 Abu5665781 Abu5665781 Abu5665781 Abu5665781 Human ppc 32 244 13.1 277 6 ABE85657 Abu5665781 Abu5665781 Abu5665781 Abu56654 Abu5665781 Abu566578 Abu566578 Abu566578 Abu566578 Abu566578 Abu566578 Abu566578 Abu566578 Abu56678 Abu56678 Abu56678 Abu56678 Abu566	187.5 10.1 360 4 AAM38965 Aam38965 Human 187.5 10.1 360 6 ABU73627 Abu73627 Abu71627 Abu71627 Abu71627 Human 187.5 10.1 360 6 ABU87961 Abu87961 Novel 187.5 10.1 360 6 ABU64276 Abu84276 Human 187.5 10.1 360 6 ABR66150 Abu66150 Human 187.5 10.1 360 6 ABR665150 Abu66150 Human 187.5 10.1 360 6 ABR665150 Abu665150 Abu765540 Human	ALIGNMENTS	RESULT 1 AAY93913 ID AAX93913 standard; protein; 353 AA.	AAV93913; 03-OCT-2000 (first entry) A human hyaluronan-binding protein, designated BM-HABP. Hyaluronan-binding protein WF-HABP; OB-HABP; BM-HABP; proliferative condition; metastasis; inflammation; ischemia; host defence dysfunction; arrhritis; multiple sclerosis; antolimmnity immune surveillance dysfunction; alterdy	Mulliple Sciences; aucolmmunicy; immune cyst. Homo sapiens. Key Misc-difference 94	Domain Misc-difference 1	Misc-difference 3 Misc-difference 3 Misc-difference 3	Misc-difference 7.10ce unspecified amino acid encoded by Misc-difference 3.25 Misc-difference 3.51 Misc-difference	MO200039166-A1. 06-JUL-2000. 20-DEC-1999; 99WO-US030 23-DEC-1998; 98US-01136 (HTMA.) HIMAN GENOME SCT	(AMNA-)
	table:	Total number of hits satisfying chosen parameters: 1586107 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : A_Geneseq_29Jan04:* 1: geneseqp1980s:* 2: geneseqp1998s:* 3: geneseqp2000s:* 4: geneseqp2001s:* 5: geneseqp2001s:* 6: geneseqp2011s:* 7: geneseqp2003as:* 7: geneseqp2003bs:* 8: geneseqp2003bs:* 7: www	dicted by chance to have a re of the result being printed, I score distribution.	Result Query DB ID Description FT FT FT FT P P P P P P P P P P P P P P	1849 99.1 353 3 AAY93913 Aay93913 1772 95.0 1394 5 AAM47684 Aam47684 Aam47684 1772 95.0 1416 6 ABG72499 Abg7249 Abg7249 1769 94.9 897 5 AbJ10586 Ab	1514.5 81.2 1431 6 AGM472498 AD672498 RAL INJERTOR INJERT	AAN93311 AA93310 AA933310 AURILLAND AA93310 AURILLAND AA93310 AURILLAND AA93310 AURILLAND AURILL	262 14.0 277 2 AAN84087 Aat280*4 INDUL INDUL INDUL 1.2 262 14.0 277 2 AAN84087 Aaw84087 Tumour ne

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02-NOV-2000; 2000US-0245320P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; vitreous humour; endocytic receptor; glycosaminoglycan; human.
                                                             proteins, known as full-length WF-HABP, WF-HABP, OE-
                                                                                                                                                                                                                                                                                                                                                                         RSPLQQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLINFLIEVLAYSNSSARGRAFLEHLIDLSIRGILFVPQNSGLGENETLSGRDIEHHLAN
                                                                                                                                                  specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OE-HABP, and BW-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis, inflammation, ischemia, host defence dysfunction, immune surveillance dysfunction, arthritis, multiple sclerosis, autoimmunity, immune
                                                                                                                                                                                                                                                                                                                       1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                                                                            1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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                                                                       HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis.
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                        The present sequence represents a hyaluronan-binding protein. The
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                  99.1%; Score 1849; DB 3; Length 353; 100.0%; Pred. No. 2.3e-184; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Hyaluronic Acid Receptor for Endocytosis, HARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM47684 standard; protein; 1394 AA
                                                                                                              Claim 11; Fig 4A-B; 457pp; English.
Tsifrina E;
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                                                                                                                                                                                                                                                                                             Matches 353; Conservative
                                                                                                                                                                                                                  dysfunction and allergy
Liau G,
                                                            New hyaluron-binding
                        WPI; 2000-452376/39.
                                                                                                                                                                                                                                                                                 Similarity
                                     N-PSDB; AAA57365
                                                                                                                                                                                                                                             Sequence 353 AA;
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Hastings GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    986 МІСРСКИКСЕСКЅНУУСРСІЛІСЕРЕДІРІ ПОТОГОВОВОТНІ 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, ABA04662, ABA04662, ABA04662, ABA04662, ABA04662, ABA04664, ABA04689, HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues; in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is human HARE
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tumour; gene therapy; human; gene; ss.
                                                                                                                                                                                                                                                                                 New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for identifying agents that inhibit binding to hyaluronic acid, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ONCGSGVVGIVDYGPRPNKSEMMDVFCYRMXDVNCTXKVGYVGDGFSYSGNLLQVLMSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1166 SLINFLIEVLAYSNSSARGRAFLEHLIDLSIRGILFVPQNSGLGENETLSGRDIEHHLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RSPLGOYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%; Score 1772; DB 5; 94.6%; Pred. No. 2.1e-175;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Fig 33; 263pp; English.
                                                                                                                                        Weigel JA
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                                                                                                                                     Zhou B,
                                                                                                                                                                                                           WPI; 2002-049271/06
                                 (ZHOU/) ZHOU B.
(WEIG/) WEIGEL J A.
(WEIG/) WEIGEL P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1394 AA;
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                                                                                                                                                                                                                                                                                                                                                       nucleic acid.
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Matches 334;
                                                                                                                                        Weigel PA,
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ABG72514 standard; protein; 1653 AA

ABG72514

ABG72514;

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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) receptor for endocytosis (HARE) or a cell that does not express tunctionally active HARE. The method involves using HA molecule, a chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The method is useful for targeting a compound, preferably a chemotherapeutic agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least one of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its surface. This second method is useful for preventing metastasis by preventing interaction between tunour cells having HA, CD or CDS coat and non-tumour cells expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This sequence encodes the human 190kDa Hyaluronan ceptor for endocytosis (HARE)
                                                                                                                                                                                                                                                                                                                                                   rgeting compounds e.g. chemotherapeutic agent to cell of subject pressing functional active hyaluronan receptor for endocytosis of HARE, using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Fig. 9A; 167pp; English.
                                                                25-APR-2002; 2002WO-US013209.
                                                                                                       25-APR-2001; 2001US-00842930.
25-APR-2001; 2001US-0286468P.
                                                                                                                                                                                                                                             Weigel PH, Weigel JA;
                                                                                                                                                                                                                                                                                       WPI; 2003-093126/08.
                                                                                                                                                                        (WEIG/) WEIGEL P H. (WEIG/) WEIGEL J A.
                                                                                                                                                                                                                                                                                                           N-PSDB; ABX13822
                       31-OCT-2002
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Sequence 1416 AA;

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1247
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                                                                                                                                                                                                                                                                  RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
                                                                                                                                          QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP
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                                                           1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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                                0; Gaps
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   Length 1416;
                             17; Indels
95.0%; Score 1772; DB 6; 94.6%; Pred. No. 2.1e-175; ive 2; Mismatches 17;
                              334; Conservative
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RESULT

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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) receptor for endocytosis (HARE) or a cell that does not express that the method involves using HA molecule, a chondroitin molecule (CD), a chondroitin sulphate (CDS) molecule, and/or a monocional antibody raised against a HA-binding domain of HARE. The camenod is useful for targeting a compound, preferably a chemotherapeutic gaent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a come of a HA coat, a CD coat and a cell expressing HARE on its surface. This second method is useful for preventing interaction between a cell having at least one of a HA coat, a CD coat and call expressing HARE on its surface. The second method is useful for preventing metastasis by preventing interaction between tumour cells having HA, CD or CDS coat and call computumour cells expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This is the amino acid sequence of a longer version continuour metable having the presence of HA, CD and CDS in a biological fluid. This is the amino acid sequence of a longer version and a continuour cells having the presence of HA, CD and CDS in a continuour cells the amino acid sequence of a longer version and a continuour cells the amino acid sequence of a longer version and a continuour cells the amino acid sequence of a longer version and a continuour cells the amino acid sequence of a longer version and a continuour cells accorded to a longer version and a cell the continuour cells accorded to a longer version and a cell the continuour cells accorded to a longer version and a cell the continuour cells accorded to a longer version and a cell the continuour cells accorded to the continuour ce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
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                                                                                                                                                                                                  Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA, CD; chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis; tumour; gene therapy; human.
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                                                                                                                                                        Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
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25-APR-2001; 2001US-0286468P.
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Conservative
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N-PSDB; ABX13823.
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1365 ONCGSGVVGIVDÝGPRPNKSEMWDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLOVLMSFP 1424
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in coding sequence"
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                                                                                                                                                                                                                                                                                                                                                                    Human, NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic; antiatreriosclerotic; antidiabetic; antiasthmatic; antiinflammatory; haemostatic; hypotensive; neuroprotective; anorectic; nootropic; antidepressant; immunosuppressive; antibacterial; antiparasitic; virucide; tranquilizer; anticonvulsant; osteopathic; analgesic; antiparkinsonian; dermatological; antiinfertility; cerebroprotective; antiaddictive.
                                                 1425 SLINFLIEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN
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                             181 SLINFLIEVLAYSNSSARGRAFLEHLIDLSIRGILFVPQNSGLGENETLSGRDIEHHLAN
                                                                                        241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI
                                                                                                                                                                   SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
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2001US-0272408P.
2001US-0285189P.
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20-APR-2001;
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WPI; 2002-666903/71. N-PSDB; ABT08489.

Rothenberg M;

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          New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease or Alzheimer's disease.
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                                                                                                                                                  The present invention provides the protein and coding sequences of several novel human proteins, designated NoWx. These can be used in the treatment of diseases such as cancer, hodgkin's disease, von Hippellindau syndrome, Alaheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia telangiectasia, leukodystrophies, addiction, anxiety, depression, besity, crohn's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     609 ONCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLLQVLMSFP
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                                                                                                                  Claim 54; Page 25; 363pp; English.
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Matches 333; Conservative
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2567 SRPLKAPPAPVTLTHTGLGAGIFFCIILVTGAVALAAYSYFRINRRTIGYQHF 2619

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1188 SLINFLITEVIAFSKSSARGQAFLKHLTDLSIRGTLFVPQNSGLPGNKSLSGRDIEHHLIN 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1068 RSPLGOYKLTFDKAXEACAXEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAXPTTYAS 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to sequences for rat and human HARE (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAA47675 and AAA47684). HARE can bind specifically to at least one of hyaluronic acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin sulphate (CS). HA is an extracellular matrix component of all tissues, in particular cartilage, skin and vitreous humour. HARE is the endocytic receptor responsible for removing HA and other glycosaminoglycans from the circulation. The present sequence is rat HARE
                                                                                                                                                                                                                                                                                                                                                                               HARE, Hyaluronic Acid Receptor for Endocytosis, hyaluronan; chondroitin; chondroitin sulphate; extracellular matrix; cartilage; skin; vitreous humour; endocytic receptor; glycosaminoglycan; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for identifying agents that inhibit binding to hyaluronic acid, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1008 MTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                              Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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                                                                                               A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Fig 21; 263pp; English.
                                                                                               AAM47675 standard; protein; 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weigel JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2001; 2001WO-US013403.
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02-NOV-2000; 2000US-0245320P.
                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 2002-049271/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZHOU/) ZHOU B. (WEIG/) WEIGEL J A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus.
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                                                                                                                                                                                                                                             22-FEB-2002
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                                                                                                                                                                        AAM47675;
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                                                             AAM47675
                                                                                                                                                                    SOURCE COURT AND THE STATE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2507 VSMFFYNDLVNGTTLÓTRLGSKLLITASÓDPLÓPVQSKFVDGRAILGWDIFASNGIIHVI 2566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     several movel human proteins, designated NoVX. These can be used in the treatment of diseases such as cancers, Hodgkin's disease, Von Hippel-Lindau syndrome. Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia cleangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, immunodeficiencies, HIV, virall, bacterial or parasitic infections, or graft, versus-host disease. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2363 RSPLGQYKLTFDKAREACANEAATWATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U; Shenoy S, Spytek KA, Gangolli E, Miller C, Boldog F, Li L; Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu X, Colman SD; Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention provides the protein and coding sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2675;
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Pred. No. 3.6e-152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 20; 363pp; English.
                                                                                                                                                                    19-JAN-2001; 2001US-0262959P.
28-FEB-2001; 2001US-0272408P.
20-APR-2001; 2001US-0285189P.
                                                                                                                                                                                                                                                                                   2001US-0308039P
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83.9%;
                                                                    19-DEC-2001; 2001WO-US050076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-666903/71.
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                                                                                                                                             19-DEC-2000;
                                                                                                                                                                                                                                                                                               26-JUL-2001;
01-AUG-2002,
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The invention describes a method of targeting a compound to a cell or tissue of an individual expressing a functionally active hyaluronan (HA) receptor for endocytosis (HARE) or a cell that does not express functionally active HARE. The method involves using HA molecule, and/or chondroitin molecule (CD). A chondroitin sulphate (CDS) molecule, and/or a monoclonal antibody raised against a HA-binding domain of HARE. The method is useful for targeting a compound, preferably a chemotherapeutic agent or a radioisotope to cell of an individual, especially a human, expressing HARE on its surface (e.g. gene therapy). Also described is a method useful for preventing interaction between a cell having at least on of a HA coat, a CD coat and CDS coat and a cell expressing HARE on its surface. This second method is useful for preventing metastasis by preventing interaction between tumour cells having HA, CD or CDS coat and cDS preventing interaction between tumour cells having HA, CD or CDS coat and contumour cells expressing HARE on its surface. The invention also describes a method useful for detecting the presence of HA, CD and CDS in a biological fluid. This is the amino acid sequence of the rat 175kDa
                       241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Targeting compounds e.g. chemotherapeutic agent to cell of subject expressing functional active hyaluronan receptor for endocytosis of HARE, by using hyaluronan, HARE, and/or monoclonal antibody that binds to HARE
                                                                                                                                                                                                                                                                                                                                                                                   Hyaluronan receptor for endocytosis; HARE; hyaluronan; HA; CD; chondroitin molecule; chondroitin sulphate; CDS; targeting; metastasis; tumour; gene therapy; rat; receptor.
                                                                                                     301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF
                                                                                                                                                                                                                                                                                                                                                   Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyaluronan receptor for endocytosis (HARE)
                                                                                                                                                                                                                           ABG72498 standard; protein; 1431 AA
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25-APR-2001; 2001US-0286468P.
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                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                             19-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp.
                                                                                                                                                                                                                                                                  ABG72498;
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                                                                                                                                                                                  RESULT 8
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1008 MTGPGKHKCECKSHYVGDGVDCEPEQLPLDRCLQDNGQCHPDASCADLYFQDTTVGVFHL 1067
                                                                                                                                                                                                1068 RSPLGQYKLTFDKAKEACAKEAATIATYNQLSYAQKAKYHLCSAGWLESGRVAYPTTYAS 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiviral; antibacterial; antifungal; antitheumatic; antithyroid; antitinaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; alevge; combined immunodeficiency; malaria; automimune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, open reading frame, ORFX, detection, cytostatic; hepatotropic, vulnerary, antipsoriatic, antiparkinsonian, nootropic, neuroprotective, antionvulsant; osteopthic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic, antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                               121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP
                                                                                                                                                                                                                                                                                                                                                                      1128 OKCGANVVGIVDYGSRANKSEMWDVFCYRMKDVNCTCKAGYVGDGFSCSGNLLQVLMSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 SLINFLIEVLAYSNSSARGRAFLEHLIDLSIRGILFVPQNSGLGENETLSGRDIEHHLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI
1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB42164 standard; protein; 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999; 99US-0127607P.
02-APR-1999; 99US-0127636P.
05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000WO-US008621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC76373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200058473-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saplens.
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Query Match
Best Local Similarity 79.3%; Pred. No. 1.9e-148;
Matches 280; Conservative 29; Mismatches 43; Indels 1; Gaps

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noortropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; cartivital, antithomatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition of the preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative clashers and isorders, proliferative disease, cardiovascular disease, disorders, osteoarchritis, graft vs. host disease, cardiovascular disease, disorders, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal hemoglobinuia, antiinflammatory disease; to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 AATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCGSGVVGIVDYGPRPNKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.2%; Score 1215.5; DB 3; Length 330; 87.2%; Pred. No. 4.2e-118; ive 4; Mismatches 30; Indels 1;
neurodegenerative disorders and cardiovascular disease.
                                                       Claim 11; Page 3007-3008; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 330 AA;
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Shimkets RA, Patturajan M, Vernet CAM, Casman SJ, Malyankar U; Shenoy S, Syytek RA, Gangolli B, Miller C, Boldog F, Li L; Taupier RJ, Kekuda R, Smithson G, Zerhusen BD, Liu K, Colman SD; Tchernev V, Si J, Edinger S, Stone D, Sciore P, Millet I;

19-JAN-2001; 2001US-0262959P. 20-APR-2001; 2001US-0272408P. 20-APR-2001; 2001US-0285189P. 20-JUL-2001; 2001US-0311266P.

(CURA-) CURAGEN CORP.

19-DEC-2001; 2001WO-US050076.

01-AUG-2002

2000US-0256619P.

19-DEC-2000;

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201
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                                                                                                                                                       202 FLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNGTTLQTRLGS 261
                                                                                                                                                                                                                                                               262 KLLITDRODP-LHPTETRCVDGRDTLEWDICASNGITHVISRXLKAPPAPVTLXHTGLGX 320
                                                                                                                                                                                                                                                                                                                  241
  61
                                                                                      62 MWDVFCYRMKDVNCTCKVGYVGDGFSCSGNLLQVLMSFPSLINFLTEVLAYSNSSARGRA
2 AATMATYNOLSYAQKAKYHLCSAGWLETGRVAYPTAFASONCGSGVVGIVDYGPRPNKSE
                                                      142 MMDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFPSLTNFLTEVLAYSNSSARGRA
                                                                                                                                                                                        122 FLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLANVSMFFYNDLVNGTXPANEGGK
                                                                                                                                                                                                                                                                                                               182 QAAHHCQPGPTXQPTETRFVDGRAILQWDIFASNGIIHVISRPLKAPPAPVTLTHTGLGA
                                                                                                                                                                                                                                                                                                                                                                   321 GIFXXIILVIGAVALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                                                                                                                                                                       242 GIFFAIILVTGAVALAAYSYFRINRRTIGFOHF 274
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Human; NOVX; single nucleotide polymorphism; SNP; anti-HIV; cytostatic;
                                                                                                                                                                                antiarteriosclerotic; antidiabefic; antiasthmatic; antiinflammatory; haemostaric; hypotensive; neuroprotective; anorectic; noctropic; antidepressant; immunosuppressive; antibacterial; antiparastic; virucide; tranquilizer; anticonvuleant; osteopathic; analgesic; antiparatinsonian; dermatological; antiinfertility; cerebroprotective;
                                                                                                                                  Human novel protein NOV1b SEQ ID NO: 4.
                                 ABJ10587 standard; protein; 2420 AA
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                           antiaddictive
                                                                                                   28-NOV-2002
                                                                   ABJ10587;
RESULT 10
                   ABJ10587
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WO200259315-A2

Homo sapiens.

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---SAGLFQQLSSRP 2413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders e.g. diabetes, Crohn's disease, atherosclerosis, cancer, Huntington's disease or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of several novel human proteins, designated NOWX. These can be used in the treatment of diseases such as cancers, Hodgkin's disease, von Hippellindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, crohn's disease, addiction, anxiety, depression, pain, obesity, crohn's disease, infertility, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2250 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.4%; Score 847; DB 5; Length 2420; 85.2%; Pred. No. 3.1e-78; tive 2; Mismatches 9; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2370 ONCGSGVVGIVDYGPRPNKSEMWDVFCYRMKG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 23-24; 363pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB83358 standard; protein; 315 AA.
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Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-666903/71.
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                                                                                                                                                                                                                                                                                                                                                          Rothenberg M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Shimkets RA, Lichenstein H, (CURA-) CURAGEN CORP. immune disorders.

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NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; estime/thronine kinase; Peutz-Jephers syndrome; cellular prolliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV9; NOV10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0166336P.
99US-0167785P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000; 2000US-0187844P.
16-NOV-2000; 2000US-00715417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000; 2000WO-US031543.
                                                                      NOV2 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200136638-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
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26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2001,
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Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and WPI: 2001-648134/74. N-PSDB; AAF87113

Fernandes E;

Vernet C,

Claim 1; Page 10-13; 141pp; English.

This sequence is the NOV2 protein. The invention relates to the NOV1-NOV16 proteins, and their coding sequences. The proteins have Cytostatic contraceptive, antiinflammatory; immunomodulatory; and cardiovascular activities. The sequences may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate NOVX expression. They may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of protein by expressing inactive proteins or to supplement the activity of protein by expressing inactive proteins or to supplement the activity of protein of protein. They are used to produce NOVX proteins, by inserting the nucleic acid into a cell and culturing it to express the protein. The DNA may be used as DNA probes in assays to detect and quantitate the presence of similar DNAs in samples, and which grained may need restorative therapy. The NOVX protein may also be used as antigens in the production of antibodies (ADS) against NOVX and in assays to identify modulators of NOVX expression and activity. The anti-NOVY Abs and antagonist are used to down regulate expression and activity. Inte dilliNOVY Abs and antagonist are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV5, NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat kinase-related disorders serine/threonine kinases, and are used to treat kinase-related disorders.

NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF) (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception).

NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (EGF) (e.g. Peutz-Jeghers syndrome, cell adhesion, growth migration, cell structure and mocility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders.

NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT syndrome and marfan syndrome

Sequence 315 AA;

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Η.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the he diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune bacamis, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing
                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiallergic, hepatotropic, antidiabetic, antifulammatory, antiuleer, vulnerary, anticonvulsant, antibacterial, antifungal, antiparasitic, cardiant, gene therapy, cancer; immune disorder, cardiovascular disorder, neurological disease, infection, human, secreted protein.
                                                                                                                                                                                                                                                                       265 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRWKG-------SAGLFQQLSSRP 308
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                                                                                                                                                        61 RSPLGQYKLIFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
                                                                           1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                           205 RSPLGQYKLTFDKAREACANEAATMATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFAS
                                                                                                                                                                                                                                    QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP
                                                                                                                145 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCADLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
                                        16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 2725; 2081pp + Sequence Listing; English.
  Length 315;
                                      Indels
                                      10;
Score 843; DB 4;
Pred. No. 3.8e-79;
2; Mismatches 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB90349 standard; protein; 1082 AA.
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  45.2%;
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                                      Matches 155; Conservative
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  Query Match
Best Local Similarity
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964 IHALASPLLAPPQPQAVLAPEAPPVAAGVGA-----VLAAGALLGLVAGALYLRARGKP 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                 21;
                                                                                                                                                                           Length 1082;
                                                                                                                                                                     35.5%; Score 661.5; DB 5; Length 39.9%; Pred. No. 2.4e-59; Live 49; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR82200 standard; protein; 2570 AA.
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Best Local S
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cestpared as common tympnatic endocretial and vascular endotherial endocretical and vascular endotherial endocretical codesupared as common tympnatic endocretial and vascular endotherial codium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) under non-reducing conditions, recognisable by a monoclonal antibody selected from the group consisting of DSW ACC 2519 or 2590. Also described: (1) a CLEVER-1 antibody; (2) a cell-free preparation comprising CLEVER-1; (3) diagnosing inflammatory diseases in a patient; (4) detecting malignant cells in a patient; (5) identifying an agent that stimulates or inhibits the binding of CLEVER-1 to cells; (6) removing malignant cells from a sample; (7) treating inflammation in a patient; (8) preventing metestasis in a patient; and (9) stimulating CLEVER-1 binding in a patient. CLEVER-1 has antiinflammatory, dermatological, antidiabetic, antisrheumatic, osteopathic, antiaschmatic, cytostatic, hepatotropic, antiarteriosclerotic, noctropic and immunosuppressive activities. The CLEVER-1, antidodies and methods from the present invention can be used for treating inflammations, diabetes, or chronic inflammatory diseases such as skin inflammations, diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 JELNTRRCECHAGYVGDGLQCLEESEPPVDRCLGQPPPCHSDAMCTDLHFQEKRAGVFHL 2212
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                                                                                                                                                                                                                                                                          New purified lymphatic endothelial glycoprotein, designated as common lymphatic endothelial and vascular endothelial receptor- (CLEVER-1), recognizable by a monoclonal antibody, useful for treating inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis, cirrhosis, cholagitis, atherosclerosis, vasculitis, thyroiditis, multiple sclerosis, myositis, ischaemia reperfusion injury or transplantation rejection, and for preventing metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ulcerative colitis and Crohn's disease), various nephritides, non-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ONCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFS-YSGNLLLQVLMSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  connective tissue diseases (such as lupus, rheumatoid arthritis, osteoarthritis), obstructive and restrictive lung diseases (such as
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09-JAN-2002; 2002US-0346288P.
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                                            (JALK/) JALKANEN S.
(IRJA/) IRJALA H.
(SALM/) SALMI M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hyaluron-binding proteins, known as full-length WF-HABP, WF-HABP, HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a hyaluronan-binding protein. The specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OE-HABP, and BM-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis, inflammation, ischemia, host defence dysfunction, immune surveillance dysfunction, arthritis, multiple sclerosis, autoimmunity, immune dysfunction and allergy
                                                                                                                                                                                   Hyaluronan-binding protein WF-HABP; OE-HABP; BM-HABP; proliferative condition; metastasis; inflammation; ischemia; bost defence dysfunction; immune surveillance dysfunction; arthritis; multiple sclerosis; autoimmunity; immune dysfunction; allergy.
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                                                                                                                                                            A human hyaluronan-binding protein, designated WF-HABP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.2%; Score 656.5; DB 3; Best Local Similarity 39.7%; Pred. No. 2.2e-59; Matches 144; Conservative 50; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                 'note= "EGF-like type 2 domain"
                                                                                                                                                                                                                                                                                               'note= "HA binding domain"
                                                                                                                                                                                                                                                                                                                         'note= "link domain"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                   AAY93911 standard; protein; 457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 2A-B; 457pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsifrina E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
(AMNA-) AMERICAN NAT RED CROSS.
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N-PSDB; AAA57363.
                        2506 TGF 2508
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348 IGF 350
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944. .353
'note= "cytochrome P450 cysteine haem-iron ligand binding
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   9
                                                                  99
                                   40 TGLNTRRCECHAGYVGDGLQCLEESEPPVDRCLGQPPPCHSDAMCTDLHFQEKRAGVFHL
                                                                                                                                  61 RSPLGOYKLTFDKAREACANEAATWATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
                                                                                                                                                                                              100 QATSGPYGLNFSEAEAACEAQGAVLASFPQLSAAQQLGFHLCLMGWLANGSTAHÞVVFPV
                                                                                                                                                                                                                                                                    121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFS-YSGNLLQVLMSF
                                                                                                                                                                                                                                                                                                           160 ADCGNGRVGIVSLGARKNLSERWDAYCFRVQDVACRCRNGFVGDGISTCNGKLLDVLAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferative condition; metastasis; inflammation; ischemia; host defence dysfunction; immune surveillance dysfunction; arthritis; multiple sclerosis; autoimmunity; immune dysfunction; allergy.
TGPGKHKCECKSHYVGDGLNC-EPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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/note= "EGF-like type 2 domain"
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note= "EGF-like type 2 domain"
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/note= "EG
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New hyaluron-binding proteins, known as full-length WF-HABP, WF-HABP, OE-HABP and BM-HABP, useful for treating proliferative conditions, metastasis, inflammation, ischemia, arthritis and multiple sclerosis.
                              note= "prokaryotic membrane lipoprotein lipid attachmentsite domain"
                                                                                                 note= "prokaryotic membrane lipoprotein lipid attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a hyaluronan-binding protein. The specification describes four hyaluronan-binding protein, known as WF-HABP, WF-HABP, OE-HABP, and BM-HABP. The polypeptides are useful for treating diseases such as proliferative conditions, metastasis, inflammation, ischemia, host defence dysfunction, immune surveillance dysfunction, arthritis, multiple sclerosis, autoimmunity, immune dysfunction and allergy
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "unspecified amino acid encoded by GAN"
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                                                                                                                                                                                                                                                                                                                                                                                               'note= "unspecified amino acid encoded by CNT"
                                                                                                                         582. .1616

note= "laminin-type EGF domain"

582. .1596

note= "EGF-like type 2 domain"

582. .1593
                                                                                                                                                                                                                                 /note= "EGF-like type 1 domain"
1663. .1676
/note= "EGF-like type 2 domain"
1747. .1760
          note= "EGF-like type 2 domain"
103. .1113
                                                            1111. .1125
/note= "EGF-like type 2 domain"
1405. .1415
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note= "EGF-like type 1 domain"
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note= "EGF-like type 2 domain"
626. .1637
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'note= "EGF-like type 2 domain"
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note= "link protein domain"
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N-PSDB; AAA57362.
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1860 ADCGNGRVGIVSLGARKNISERWDAYCFRVQDVACRCRNGFVGDGISTCNGKLIDVLAAT 1919
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                                                                61 RSPLGQYKLIFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
                                                                                                                                 121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFS-YSGNLLQVLMSF 179
                                                                                                                                                                                                    180 PSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLA 239
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                                                                                      TGPGKHKCECKSHYVGDGLNC-EPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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Search completed: March 30, 2004, 15:37:46 Job time: 61 secs

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Gaps

21;

Query Match 35.2%; Score 656.5; DB 3; Length 2157; Best Local Similarity 39.7%; Pred. No. 2.2e-58; Matches 144; Conservative 50; Mismatches 148; Indels 21;

Sequence 2157 AA;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 30, 2004, 15:37:50 ; Search time 45 Seconds (without alignments) 2475.065 Million cell updates/sec

US-09-466-778B-11

1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1017041 segs, 315518202 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL 25:* 1: sp_archea:* 2: sp_bacteria:* fungi:* Database :

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:* sp_unclassified:* sp_rodent:*
sp_virus:*
sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_organelle:* sp_phage:* sp_archeap:* sp plant:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	09H7H7	Q86UR4	QSTES1	Q8WWQ8	QBIUG9	07Z5N9	Q9NRY3	L QBCFM6	L QBBM87	L Q8R4U0	Q9UF98	L QBKOK6	L QBR4Y4	OBINHI	93072	Q9NY15	
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	Score	1772	1772	1772	1772	1772	1772	1769	1514.5	1487	1487	1480	664.5	664.5	661.5	661.5	652.5	
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homo	Q96S86 Q80XX3	4 11	359		187.5	19 20
Q864u4 bos taurus O8vc09 mus musculu	Q864U4 O8VC09	6	500	34.5	643 324.5	17

PRT; 1192 AA PRELIMINARY; Q9H7H7 09H7H7;

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606, Created)
Last sequence update)
Last annotation update) FLJ00112 protein (Fragment). FLJ00112. 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25, Homo sapiens (Human).

SEQUENCE FROM N.A. TISSUE=Spleen;

Ohara O., Nagase T., Kikuno R., Okumura K.; Instance of a long cDNA clone isolated from human "The nucleotide sequence of a long cDNA clone isolated from human Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AK024503; BAB15793.1; -. HSSP; P98066; 1TSG.

GO; GO: 0005540; F:Byaluronic acid binding; IEA.
GO; GO: 0005198; F:Btructural molecule activity; IEA.
GO; GO: 0007155; P:cell adhesion; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006219; Laminin_EGF.

PRINTS; PRO0011; EGFLAMININ.
PRINTS; PR01265; LINKMODULE.
PRODOM; PD000918; Link; 1.
SMART; SM00181; EGF; 9.
SMART; SM00554; FASI; 3.
SMART; SM00445; LINK; 1. Pfam; PF00008; EGF; 7. Pfam; PF02469; Fasciclin; 2. Pfam; PF00193; Xlink; 1.

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FLJ00122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
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Zhou B., McGary C.T., Weigel J.A., Saxena A., Weigel P.H.;
"Purification and molecular identification of the human hyaluronan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                             1 95.0%; Score 1772; DB 4; Length 1192; Similarity 94.6%; Pred. No. 4e-158; Onservative 2; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                      SEQUENCE 1192 AA; 128738 MW; 5966BED4B83BD9C1 CRC64;
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GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005540; F:byaluronic acid binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:setructural molecule activity; IEA.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hyaluronan receptor for endocytosis (Fragment)
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PS00022; EGF_1; 4.
PS01186; EGF_2; 8.
PS50213; PSAS1; 3.
PS01248; LAMININ TYPE EGF; 2.
domain; Laminin EGF-like domain.
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InterPro; IPR001801; EGF Ca.
InterPro; IPR00209; EGF like.
InterPro; IPR005010; IEGF.
InterPro; IPR005010; IEGF.
InterPro; IPR0016539; Link.
InterPro; IPR001673; S. mold_repeat.
Pfam; PF00008; EGF; 8.
Ffam; PF00193; Xlink; 1.
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Glycobiology 13:339-349(2003).
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PROSITE; I
EGF-like o
         PROSITE;
PROSITE;
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Jiknya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.0%; Score 1772; DB 4; Length 1416; 94.6%; Pred. No. 5.1e-158; tive 2; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAĪN <1 1416 190 kDa hyaluronan receptor for endocytosis
SEQUENCE 1416 AA; 154089 MW; 85A216D38E3B10DE CRC64;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DR ProDom; PD000918; Link; 1.

DR SMART; SM00181; EGFLAMININ.

DR SMART; SM00181; EGF, 11.

SMART; SM00191; EGF, 11.

SMART; SM00192; EGF CA; 4.

R SMART; SM00454; FASI; 4.

R PROSITE; PS00022; EGF 1; 4.

PROSITE; PS01186; EGF 1; 4.

PROSITE; PS01186; EGF 1; 4.

PROSITE; PS01186; EGF 1; 4.

PROSITE; PS01248; LAMININ_TYPE_EGF; 2.

RECEPLOT.
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Best Local Similarity 94.6*
Matches 334; Conservative
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Query Match
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                              95.0%; Score 1772; DB 4; Length 1736; 94.6%; Pred. No. 6.9e-158; ative 2; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                   1736 AA; 187887 MW; 50982047E43925F2 CRC64;
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Last annotation update)
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InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002049; Link.
Pfam; PF00408; EGF; 12.
Pfam; PF00408; EGF; 12.
Pfam; PF00109; Klink; 1.
PRINTS; PR00101; EGFLAMININ.
ProDom; PD000918; Link; 1.
SWART; SW0048; Link; 1.
SWART; SW00454; FASI; 5.
SWART; SW00454; FASI; 5.
PROSITE; PS01022; EGF_1; 4.
PROSITE; PS01186; EGF_2; 12.
PROSITE; PS01186; EGF_2; 12.
PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
EGF-1ike domain.
NON TER
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SEQUENCE 1736 AA; 187887 MW; S0982047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 334; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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"PEBL-1, a novel scavenger receptor with in vitro bacteria-binding and angiogenesis modulating activities.";

J. Biol. Chem. 27:34264-3270(2002).

EMBL, AB052958; BAC15608.1;

Genew; HGNC:18629; STAB2.

GO, GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005500; F:hyaluronic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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R InterPro; IPR000782; BIGH3 FAS1.
R InterPro; IPR006209; EGF like.
R InterPro; IPR006209; EGF like.
R InterPro; IPR0062049; Laminin_EGF.
R InterPro; IPR000249; Laminin_EGF.
R Pfam; PF00008; EGF; 16.
R Pfam; PF001093; Xlink; 1.
R PFam; PF001093; Xlink; 1.
R PROMIS; RM0011; EGFLAMININ.
R PRODOM; PD000918; Link; 1.
R PROMOHS; EGF, 20.
R SMART; SM00184; EGF, 20.
R SMART; SM00445; Link; 1.
R PROSITE; PS01024; EGF 1; 7.
R PROSITE; PS01248; LAMININ TYPE EGF; 2.
R PROSITE; PS01248; LAMININ TYPE EGF; 2.
R PROSITE; PS01248; LAMININ TYPE EGF: 2.
R EGF-like domain, Laminin EGF-like domain.
C SEQUENCE 2551 AA; 276992 MW; 60A44651CCC2BE69 CRC64;
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Last annotation update)
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01-WAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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us-09-466-778b-11.rspt

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GO; GO:0005540; F:byaluronic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
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SMART; SMO0554; FAS1; 3.
SMART; SMO0454; LINK; 1.
PROSTIE; PSO0022; EGF 1; 2.
PROSTIE; PSO1186; EGF 2; 4.
PROSTIE; PSO1213; FASI; 3.
PROSTIE; PSO1249; LAMININ_TYPE_EGF; 1.
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Pfam; PF02469; Fasciclin; 2.
Pfam; PF0193; Xlink; 1.
PRINTS; PR01265; LINKWODULE.
ProDom; PD000918; Link; 1.
                                                                   Query Match
Best Local Similarity 94.64
Matches 334; Conservative
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Q9NRY3;
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"FEX2, a novel cell adhesion molecule of Fas-1 superfamily mediates
cell-cell interaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2443 SRPLKAPPAPVTLTHTGLGAGIFFAIILVTGAVALAAYSYFRINRRTIGFQHF 2495
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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R GO; GO:0004867; F:serine protease inhibitor activity; IEA. GO; GO:0001155; P:serine protease inhibitor activity; IEA. GO; GO:0001155; P:serll adhesion; IEA.

R InterPro; IPR001981; EGF Ca.
R InterPro; IPR001881; EGF Ca.
R InterPro; IPR002049; Laminin EGF.
R InterPro; IPR002049; Laminin EGF.
R InterPro; IPR002049; Laminin EGF.
R InterPro; IPR00019; EGF 16.
R InterPro; IPR00019; EGF: 16.
R Ffam; PF00109; Fasciclin; 6.
R Ffam; PF00109; Fasciclin; 6.
R Frono; PF00019; EGF.AMININ.
R FRINTS; PR00119; EGF.CA; 8.
R SWART; SW0018; EGF.CA; 8.
R SWART; SW0018; EGF.CA; 8.
R SWART; SW0018; EGF.Lam; 5.
R SWART; SW00445; Link; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 95.0%; Score 1772; DB 4; Length 2551; Best Local Similarity 94.6%; Pred. No. 1.2e-157; Matches 334; Conservative 2; Mismatches 17; Indels 0;
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Last annotation update)
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PROSITE; PS01186; EGF_2; 16.
PROSITE; PS501213; PS31; 7.
SP0121E; PS01248; LAMININ TYPE EGF; 2.
SEQUENCE 2551 AA, 277026 MW, 3ADDF.
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01-OCT-2003 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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2203 RSPLGQYKLTFDKAREACANEAATMATYNQLSYAQKAKYHLCSAGWLETGRVAYPTAFAS 2262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
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                                                                                                                                                                    Length 2551;
                                                                                                                                                       95.0%; Score 1772; DB 4; Length 2. 94.6%; Pred. No. 1.2e-157; Live 2; Mismatches 17; Indels
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AY311388; AAP74958.1; -. SEQUENCE 2551 AA; 276986 WW; 3ACB6A6C3CB60044 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 01-00T-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)

Tao Q., Zhang W., Cao X.;
"Molecular cloning and characterization of human FELL sharing homology with CD44.";
Submitted (1707-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF160476; AAF82398.1; -.

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PROSITE; PS01022; EGF 1; 3.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS50213; FAS1; 4.
PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
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                                                                                                                  489 MIGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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                                                                                                  1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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                                                                                                                                                                                                                                                                                                                                                         729 VSMFFYNDLVNGTTLQTRVGSKLLITASQDPLQPTETRFVDGRAILQWDIFASNGIIHVI
                                                                       Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley;

XX MEDLINE=22169209; PubMed=12181351;

XX Zhou B., Weigel U.A., Saxena A., Weigel P.H.;

Zhou B., Weigel U.A., Saxena A., Weigel P.H.;

Zhou B., Weigel U.A., Saxena A., Weigel P.H.;

YY aluronan Receptor for Endocytosis.";

Molecular Cloning and Functional Expression of the Rat 175-kDa Hyaluronan Receptor for Endocytosis.";

Mol. Biol. Cell 13.2853-2868(2002).

ROS GO:0005540; Fireceptor activity; IEA.

GO: GO:0005540; Fireceptor activity; IEA.

GO: GO:000540; Fireceptor activity; IEA.

GO: GO:000198; Fireceptor activity; IEA.

InterPro: IPR00C6209; EGF like.

RINTERPRO: IPR00C6209; EGF like.

RINTERPRO: IPR00C938; Link.

DR Ffam; PF00008; EGF; J.

REAM; PF00008; EGF; J.

REAM; PF00008; Link; 1.

REAM; PR00139; Alink; 1.

REAM; PR00139; Alink; 1.

REAM; ROMO149; EGF CA; 2.

SWART; SM00149; EGF CA; 2.

SWART; SM00149; FASI; 4.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amoutation update)
Hyaluronan receptor for endocytosis HARE precursor (Fragment).
                                        94.9%; Score 1769; DB 4; Length 897; 94.3%; Pred. No. 5.2e-158; Live 3; Mismatches 17; Indels
                897 AA; 97585 MW; EB920AF36101E388 CRC64;
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                                                                    Matches 333; Conservative
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                                                        Similarity
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EGF-like domain.
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                SEQUENCE
                                           Query Match
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Q8CFM6
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STRAIN-C57BL/6J; TISSUE-Diencephalon;

XM MEDLINE-22354683; PubMed=12466851;

RA THE FANTOM Consortium,

RA THE FANTOM Consortium,

RA THE FANTOM Consortium,

RA THEN GROWNE EXPLOYATION Research Group Phase I & II Team;

RA THEN GROWNE EXPLOYATION RESEARCH GROUP Phase I & II Team;

RA THOUSE OF THE MOUSE TRANSCRIPTION OF CO.770 full-length CDMS.";

RA MAILYSIS of the mouse transcriptome based on functional annotation of CO.770 full-length CDMS.";

RE MALUE 420:563-573(2002).

RE MALUE 420:563-573(2002).

RO, GO:0005540; F:hyaluronic acid binding; IEA.

RO, GO:0005540; F:hyaluronic acid binding; IEA.

RO, GO:0005540; F:hyaluronic acid binding; IEA.

RO, GO:0005785; P:cell adhesion; IEA.

RO, GO:0007785; B:cell adhesion; IEA.

RO, GO:000782; BIGH3 FASI.

RITEFPCO; IPRO06209; EGF II.Re.

BR INTERPCO; IPRO06209; Laminin_EGF.

RITEFPCO; IPRO060398; Liminin_EGF.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
                                                                                                                             Ouery Match 81.2%; Score 1514.5; DB 11; Length 1431; Best Local Similarity 79.3%; Pred. No. 1.1e-133; Matches 280; Conservative 29; Mismatches 43; Indels 1; (
                                       1
1431 AA; 155914 MW; 3340A8F7AF366722 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to CD44-like precursor FELL (Fragment)
Mus musculus (Mouse).
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Pfam; PF02469; Fasciclin; 2.
Pfam; PF00193; Xlink; 1.
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MEDIJNE=21818465; PubMed=11829752;
Politz O., Gratchev A., McCourt P.A.G., Schledzewski K., Guillot P., Johansson S., Svineng G., Franke P., Kannicht C., Kzhyshkowska J., Longati P., Velten F.W., Johannson S., Goerdt S.;
"Stabilin-1 and -2 constitute a novel family of fasciclin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784 SEPLKAPPTAATAAHSGLGTGIFCAVVLVTGAIALAAYSYFRINORTTGFRRF 836
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                            79.7%; Score 1487; DB 11; Length 894; 77.9%; Pred. No. 2.3e-131; Live 32; Mismatches 44; Indels 2.
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GO; GO:0003779; F:actin binding; IEA.
GO; GO:0005540; F:nycluronic acid binding; IEA.
GO; GO:0005196; F:nycluronic acid binding; IEA.
GO; GO:0007155; P:ectl adhesion; IEA.
InterPro; IPR001589; Actbind actin.
InterPro; IPR005209; EGF like.
InterPro; IPR005209; EGF like.
InterPro; IPR005209; EGF like.
InterPro; IPR00549; Laminin_EGF.
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Stabilin-2.
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Biochem. J. 362:155-164(2002).
EMBL; AF364951; AAL91684.2; -.
                                                                                                                                                                                                                                                                                                                                                              al Similarity 77.99
275; Conservative
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Best Local
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Q8R4U0
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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2151 MTGPGKQKCECKSHYVGDGRDCEPEQLPLDRCLQDNGQCHPDANCVDLHFQDTTVGVFHL 2210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Testis;
Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133021; CAB61358.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.7%; Score 1487; DB 11; Length 2559; Best Local Similarity 77.9%; Pred. No. 1e-130; Matches 275; Conservative 32; Mismatches 44; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2559 AA; 277530 MW; 1C9855AD61EFF015 CRC64;
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GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR000762: BIGH3 FAS1.
InterPro; IPR006209; BGF like.
InterPro; IPR006210; IEGF.
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1069 AA.
                                                                                                                                                                                                                                                                         PROSITE; PS00019; ACTININ 1; 1.
PROSITE; PS00022; EGF 1; 7.
PROSITE; PS01186; EGF 2; 16.
PROSITE; PS50213; FASI; 7.
PROSITE; PS01248; LAMININ_TYPE_EGF; 2.
EGF-like domain.
InterPro; IPR000538; Link.
Pfam; PF00008; EGF; 13.
Pfam; PF02469; Fasciclin; 6.
Pfam; PF00193; Xlink; 1.
PRINTS; PR0011; EGFLAMININ.
                                                                                                                                                    ProDom; PD000918; Link; 1. SMART; SM00181; EGF; 21. SMART; SM00554; FAS1; 7. SMART; SM00445; LINK; 1.
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HSSP; P98066; 1TSG.
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Homo sapiens (Human)
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Stabilin-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 SLINFLIEVLAYSNSSARGRAFLEHLIDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          817 ONCGSGVVGIVDYGPRPNKSEMWDVFCYRWKG-------SAGLFQQLSSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861 CIS-------RIPDDLSIRGILFVPQNSGLGENEILSGRDIEHHLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 VSMFFYNDLVNGTTLQTRLGSKLLITASQDPLQPTETRFVDGRAILQWDIFASNGIIHVI
                                                                                                                                                                                                                                                                                                                     1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                           Gaps
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        R InterPro; IFROGOSS; Lank.

R Pfam; PF00008; EGF; 7.

R Pfam; PF00193; Xlink; 1.

R Pfam; PF00193; Xlink; 1.

R PRINTS; PR0011; EGFLAMININ.

R PRINTS; PR01265; LINKAODULE.

R PRINTS; PR01265; LINKAODULE.

R SWART; SM0018; EGF; 8.

R SWART; SM0018; EGF; 8.

R SWART; SM0021; EGF; 1.

R PROSITE; PS01026; EGF; 1.

R PROSITE; PS01186; EGF 1; 2.

R PROSITE; PS01186; EGF 1; 2.

R PROSITE; PS01186; EGF 2; 5.

R PROSITE; PS01248; LAMININ TYPE EGF; 1.

R PROSITE; PS01248; LAMININ TYPE EGF; 1.

R PROSITE; PS01248; LAMININ TYPE EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                           27; Indels 36;
                                                                                                                                                                                                                                    SEQUENCE 1069 AA; 115666 MW; 04B0960932164D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (UIN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (UIN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC031166; AH331166.1;
GO; GO:0005198; F: Structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR006782; BISH3; FASI.
InterPro; IPR006209; EGF 17ke.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                              79.4%; Score 1480; DB 4;
81.0%; Pred. No. 1.4e-130;
iive 4; Mismatches 27;
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InterPro; IPR002049; Laminin_EGF
                                                                                                                                                                                                                                                                             al Similarity 81.03
286; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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Best Local S
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1000 ANFSTFYGMLLGYANATQRGLEFMDFLEDELTYKTLFVPVNKGFVDNMTLSGPDLELHAS 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RSPLGQYKLTFDKAREACANEAATWATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFS-YSGNLLQVLMSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 PSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 NVSMFFYNDLVNGTTLQTRLGSKLLITDR---QDPLHPTETRCVDGRDTLEWDICASNGI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 THVISRXLKAP------PAPVTLXHTGLGXGIFXXII--LVTGAVALAAYSYFRIN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TGPGKHKCECKSHYVGDGLNC-EPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/c; TISSUE=Liver;
STRAIN=BALB/c; TISSUE=Liver;
MEDLINE=21818465; PubMed=11829752;
Politz O., Gratchev A., McCourt P.A.G., Schledzewski K., Guillot P., Johansson S., Svineng G., Franke P., Kannicht C., Kzhyshkowska J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 1238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.6%; Score 664.5; DB 11; Length 39.9%; Pred. No. 1.9e-53; vative 48; Mismatches 145; Indels
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Last sequence update)
Last annotation update)
                                                                                                                                                                      R SMART; SMO018; Link; 1.

R SMART; SMO0181; EGF; 11.

R SMART; SMO054; FAS1; 3.

R SMART; SMO045; LINK; 1.

PROSITE; PS00022; EGF_1; 4.

PROSITE; PS01248; EGF_2; 10.

PROSITE; PS01248; LAMININ TYPE_EGF; 2.

PROSITE; PS01248; LAMININ TYPE_EGF; 2.

PROSITE; PS01244; LINK; 1.

RGF-Like domain.
InterPro; IPR000539; Link.
InterPro; IPR0008; EGF; 8.
Pfam; PF00008; EGF; 8.
Pfam; PR02469; Fasciclin; 2.
Pfam; PF00193; Xlink; 1.
PRINTS; PR0011; EGFAMININ.
PRINTS; PR01265; LINKMODULE.
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 146; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2452 IHALASPILMPPQTRAVLGSEPPPVAL---SLGVVVTSGTLLGLVAGAL-----YLRAR 2502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2393 NATFLSIN-ASRĞTLLPAHSGLSLFİSDTGPDNTSLVPLAPGAVVVSHVIVWDİMAFNGİ 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 NVSMFFYNDLVNGTTLQTRLGSKLLITDR---QDPLHPTETRCVDGRDTLEWDICASNGI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
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Longati P., Velten F.W., Johannson S., Goerdt S.;
"Stabilin-1 and -2 constitute a novel family of fasciclin-like
hyaluronan receptor homologues.";
Biochem. J. 362:155-164(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.6%; Score 664.5; DB 11; Length Best Local Similarity 39.9%; Pred. No. 5.5e-53; Matches 146; Conservative 48; Mismatches 145; Indels
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                                                                                                                                             Biochem. J. 362:155-164(2002).
EMBL; AF290914; AAL91671.2; -.
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QBIUH1; QBIUH1; 01-MAR-2003 (TrEMBLrel. 23, Created)

RESULT 14 Q81UH1 ID Q81UH AC Q81UH DT 01-MA

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SEQUENCE FROM N.A.
MEDILINE-2220616; PubMed=12077138;
Adachi H., Tsujimoto M.;
"FEEL-1, a novel scavenger receptor with in vitro bacteria-binding and
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                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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23, Last sequence update)
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R PROSITE; PS01186; EGF 2; 16.
R PROSITE; PS01186; EGF 2; 16.
R PROSITE; PS01248; LAMININ TYPE_EGF; 2.
PROSITE; PS01241; LINK; 1.
01-MAR-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;

MEDLINE=97191544; PubMed=9039502;

MEDLINE=97191544; PubMed=9039502;

Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O.,

Tanaka A., Kotani H., Miyajima N., Nomura N.; Kawarabayasi Y., Ohara O.,

"prediction of the coding sequences of unidentified human genes. VI.

the coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
analysis of cDNA clones from cell line KG-1 and brain.";

BMBL: D87433; BAA13277.2; -.

HSSP; P98066; ITSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Gaps
                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.5%; Score 661.5; DB 4; Length 2 Best Local Similarity 39.9%; Pred. No. 1.1e-52; Matches 145; Conservative 49; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2589 AA; 277512 MW; 86F996423001C756 CRC64;
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GGGGC0005196; F: Byaluronic acid binding; IEA.

GG; GG:0005196; F: Structural molecule activity; IEA.

GG; GG:0005196; F: Structural molecule activity; IEA.

GG; GG:0005196; F: Structural molecule activity; IEA.

GG; GG:00051196; P: Cecll adhesion; IEA.

GG; GG:00061196; P: Cecll adhesion; IEA.

InterPro; IPR00128; Cytcochrome P450.

InterPro; IPR001209; EGF like.

InterPro; IPR002049; Laminin_EGF.

InterPro; IPR002049; Laminin_EGF.

Pfam; PF000409; EGF; 11.

R Fam; PF00109; Klink; 1.

R PROSITE; PS00021; EGF; 25.

R PROSITE; PS00022; EGF 1; 7.

R PROSITE; PS001249; LAMININ TYPE_EGF; 2.

R PROSITE; PS01146; EGF 2; 16.

R PROSITE; PS01149; LAMININ TYPE_EGF; 2.

R PROSITE; PS01149; LAMININ TYPE_GGF; 2.

R PROSITE; PS01149; LAMININ TYPE_GGF; 2.
                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                PRT; 2589 AA.
                                                                                                                                                                                                         Hypothetical protein KIAA0246 (Fragment).
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NON TER 1 1 SEQUENCE 2589 AA; 277512 MW: 86F99
                                                                                                                PRELIMINARY;
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2506 MGF 2508
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Search completed: March 30, 2004, 15:42:31 Job time : 48 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 30, 2004, 15:34:05 ; Search time 17 Seconds
 (without alignments)
 1081.221 Million cell updates/sec Run on:

Title: Perfect score:

US-09-466-778B-11 1865 1 MTGPGKHKCECKSHYVGDGL.....ALAAYSYFRINRKTIGFXHF 353 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt 42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	008859 mus musculu p98065 oryctolagus p88066 homo sapien P07898 gallus gall Q28343 canis famil P07898 gallus gall Q28343 canis famil P07894 rattus norv P13608 bos taurus P03994 rattus musculu Q28391 equus cabal Q9gzv7 homo sapien P55252 bos taurus P07354 gallus gall Q61282 mus musculu Q99esm3 mus musculu Q99esm3 mus musculu Q99esm3 rattus norv P16394 homo sapien P16112 homo sapien P16112 homo sapien P16112 homo sapien P16112 homo sapien P55066 mus musculu Q29011 sus scrofa P55067 rattus norv Q28662 bos taurus Q2862 mus musculu P811282 bos taurus Q61361 mus musculu P81282 bos taurus Q61361 mus musculu P81282 bos taurus Q61361 mus musculu P81282 bos taurus Q61361 mus musculu P13611 mus musculu P13611 mus musculu
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Score	264 446 262 262 262 262 263 263 263 26

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ALIGNMENTS

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                                                                                                                                                                                                                                            52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQXAKYHLCSAGWLETGR 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feng P., Liau G.;
"Identification of a novel serum and growth factor-inducible gene in "Vascular smooth muscle cells.";
J. Biol. Chem. 268:9387-9392(1993).
                                                                                                                                                                                                                  Gaps
TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                    BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor-inducible protein TSG-6 precursor (TNF-stimulated gene 6 protein) (Hyaluronate-binding protein FS4).
TNFAIRE OR TSG6 OR PS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBROR P., Liau G.;
J. Biol. Chem. 268:21453-21453(1993).
-!- FUNCTION: Possibly involved in cell-cell and cell-matrix interactions during inflammation and tumorgenesis.
-!- TISSUE SPECIFICITY: Vascular smooth muscle cells.
                                                                                                                                                                                    Length 275;
                                                                                                                                                                                                                                                                                                                            112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                 43; Indels
                                                                                                                                    -LINKED (GLCNAC. . .) (PC 1CD247228260B8F9 CRC64;
                                                                                                                                                                               14.2%; Score 264; DB 1;
43.3%; Pred: No. 4.7e-16;
tive 16; Mismatches 43;
                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- DEVELOPMENTAL STAGE: Fetal.
-i- INDUCTION: By serum and growth factor.
-i- SIMILARITY: Contains 1 link domain.
-i- SIMILARITY: Contains 1 CUB domain.
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MEDLINE=93252803; PubMed=8098034;
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                                                                                                                                                    30924 MW;
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InterPro, IPR000859, CUB.
InterPro, IPR000538, Link.
                                                                                                                                                                                                                 45; Conservative
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247
127
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161
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H
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Lee T.H., Wisniewski H.-G., Vilcek J.;
An novel secretory tumor necrosis factor-inducible protein (TSG-6):
a member of the family of hydluronate binding proteins, closely
related to the adhesion receptor CD44.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loughlin J., Day A.J.,
"A novel allelic variant of the human TSG-6 gene encoding an amino acid difference in the CUB module. Chromosomal localization, frequency analysis, modeling, and expression.";
J. Biol. Chem. 277:15354-15362 (2002).
                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLORAC. . .) (POTENTIAL).
N-LINKED (GLORAC. . .) (POTENTIAL).
W, 3BDC5D9A24B2F75A CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cordell M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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MEDLINE=21975206; PubMed=1188477;
Nentwaich H.A., Mustafa Z., Rugg M.S., Marsden B.D., Cordell M.;
Mahoney D.J., Jenkins S.C., Dowling B., Fries E., Milner C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P98066, Q8WW19;
01-FFB-1996 (Rel. 33, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor-inducible protein TSG-6 precursor (TNF-
stimulated gene 6 protein) (Hyaluronate-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 VGYPIVKPGSNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAKEC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 43.3%; Pred. No. 4.7e-16; nes 45; Conservative 16; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.2%; Score 264; DB 1;
                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                       Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                 127 BY
103 BY
161 BY
210 BY
118 N-
118 N-
258 N-
                      Pfam, PF00193, Xlink, 1.
PRINTS, PR01265, LINKMODULE.
ProDom, PD000918, Link, 1.
                                                                                                    SMART; SM00042; CUB; 1.
SMART; SM00445; LINK; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01241; LINK; 1
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Pfam; PF00431; CUB; 1.
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276 AA;
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Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Makeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalaka U.S. Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6.
LINK.
                                                                                                                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 36-133.
MEDLINE=96390850; PubMed=8797823;
Kohda D., Morton C.J., Parkar A.A., Hatanaka H., Inagaki F.M.,
Campbell I.D., Day A.J.;
"Solution structure of the link module: a hyaluronan-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       involved in extracellular matrix stability and cell migration."; cell 86:767-775(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Polymorphism; 3D-structure.
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GO; GO:0004895; F:cell adhesion receptor activity; TAS.

GO; GO:0007540; F:hyaluronic acid binding; TAS.

GO; GO:0007165; P:cell-cell signaling; TAS.

R GO; GO:0007165; P:cell-cell signaling; TAS.

R GO; GO:0007165; P:signal transduction; TAS.

R InterPro; IPR000859; Unik.

R Pfam; PF00193; Xilnk.

R Pfam; PF00193; Xilnk; 1.

R PRINTS; RR01265; LINKMODULE.

R PRART; SM00445; LINK; 1.

DR SMART; SM00445; CUB; 1.

DR SMART; SM0180; CUB; 1.

DR PROSITE; PS01180; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interactions during inflammation and tumorgenesis.
                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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-!- SIMILARITY: Contains 1 link domain.
-!- SIMILARITY: Contains 1 CUB domain.
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EMBL; AJ421518; CAD13434.1; -.
EMBL; AJ419936; CAD12353.1; -.
EMBL; BC030205; AAH30205.1; -.
PIR; A41735; A41735.
PDB; 1078; 07-NOV-03.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Li H., Schwartz N.B., Vertel B.M.;
"cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core
protein and identification of a stop codon in the aggrecan gene
associated with the chondrodystrophy, nanomelia.";
J. Biol. Chem. 268:23504-23511(1993).
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Krueger R.C. Jr., Fields T.A., Mensch J.R. Jr., Schwartz N.B.;
"Chick cartilage chondroitin sulfate proteoglycan core protein.
Nucleotide sequence of cDNA clone and localization of the S103L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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"Molecular cloning of chicken aggrecan. Structural analyses.";
Biochem. J. 288:903-910(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 VGYPIVKPGPNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAKEC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
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BY SIMILARITY.
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MEDLINE=93111968; PubMed=1339285;
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHONDRODYSTROPHY) CHARACTERIZED BY SHORTERED AND MALFORMED LIMBS.
AGGRECAN IS TRUNCATED AT ITS C-TERMINAL IN THE CS-2 BINDING DOMAIN
AND IS NOT ANYMORE SECRETED FROM THE CHONDROCYTES.
SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 4 link domains.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 GCT-ype lectin family domain.
SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: Two globular domains, Gl and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus. Gl contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B, motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroltin sulfate (CS) attachment domains lie between G2 and G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains, W.-linked and O-linked oligosaccharides.
DISBASE: DEFECTS IN AGCI ARE THE CAUSE OF NANOWELLA, A LETHAL CONNECTIVE TISSUE DISORDER AFFECTING CARTILAGE DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                      MEDLINE=86259736; PubMed=3460082;

MEDLINE=86259736; PubMed=3460082;

Sai S., Tankar T., Kosher R.A., Tanzer M.L.;

"Cloning and sequence analysis of a partial cDNA for chicken cartilage proteoglycan core protein.";

Proc. Natl. Acad. Sci. U.S.A. 83:5081-5085 (1986).

-!- FUNCTION: This proteoglycan is a major component of extracellular matrix of cartilagenous tissues. A major function of this protein is to resist compression in cartilage. It binds avidly to hyaluronic acid via an amino-terminal globular region. May play a regulatory role in the matrix assembly of the cartilage.
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                               SEQUENCE OF 1894-2109 FROM N.A.
BADLINES-89008500; PubMed=3170613;
Tanaka T., Har-El R., Tanzer M.L.;
"Partial structure of the gene for chicken cartilage proteoglycan
                                                                                                                       Primorac D., Stover M.L., Clark S.H., Rowe D.W.; "Molecular basis of nanomelia, a heritable chondrodystrophy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                  SEQUENCE OF 1492-1610 FROM N.A.
STRAIN=White leghorn; TISSUE=Chondrocytes;
MEDLINE=95128519; PubMed=7827752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoId=P07898-2; Sequence=VSP_003073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P07898-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                         core protein.";
J. Biol. Chem. 263:15831-15835(1988).
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EMBL; S74657; AAC60751.1; -.
EMBL; S74656; AAC60751.1; JOINED.
EMBL; J04028; AAA68719.1; -.
MEDLINE=94107258; PubMed=8280087;
                 Chandrasekaran L., Tanzer M.L.;
Biochem. J. 296:885-887(1993).
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ALTERNATIVE PRODUCTS:
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BGF-LIKE.

C-TYPE LECTIN.
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CS-2.
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HSSP, P08709, 1BF9.
InterPro; IPR002353 Antifreezell.
InterPro; IPR000125; Asx_hydroxyl_S.
InterPro; IPR000142; EGF_2.
InterPro; IPR000442; EGF_2.
InterPro; IPR001481; EGF_72.
InterPro; IPR001109; IGF_1ike.
InterPro; IPR001109; IGF_1ike.
InterPro; IPR001309; IGF_Iike.
InterPro; IPR001309; IGCIIn_C.
InterPro; IPR00334; GGXXGG.
InterPro; IPR003324; GGXXGG.
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G1-B.
G1-B'.
G2-B.
G2-B'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00009; EGF; 1.
Pfam; PF00047; ig; 1.
Pfam; PF00059; lectin c; 1.
Pfam; PF00139; SGXXSG; 56.
Pfam; PF00139; SGXXSG; 56.
Pfam; PF00193; Xiink; 4.
PRINTS; PR001265; ANTIFREEZEII.
PRINTS; PR001265; ININMODULE.
ProDom; PD000918; Link; 4.
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194 OCDAGWLADQTVRYPIHLPRERCYGDKDEFPGVRTYGVRETDETYDVYCYAEQMQGK--- 250
                                                                                                                                                                                                                                                                                                                       57 VFHLRSPLGQYKLJFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                                                                                                                                                              | | : | : | : | TSVIVETASPREENVIRBELIGIWAVPEEVITSVSGTAF---TIGMAEVSVEEALAVTA 482
                                                                                                                                                                                                                                                                                                                                     117 AFASQNCGSGVVGI--VDYGPR-----PNKSEMWDVFCYRMKDVNC-----TXKVG-YV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SGNLLQVLMSFPSLTNFL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSAFTIQTUTQTEVELPLPRNVTEEEARGSIATLEPMEITATATELYEAFTVLPDL--FA 425
                                                                                                                                                                                                                                                                 ----DAKCVDLHFQDTTVG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUENCE FROM N.A. TAGAMS N.E., Kwok S.X.F., Huang D., Fueloep C.; and T. F., Adams M.E., Kwok Geduced amino acid sequence of aggrecan canine cartilage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
                                                                                                                                                                                                        ; Score 175; DB 1; Length 2109;
; Pred. No. 4.8e-07;
31; Mismatches 116; Indels 98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryoţa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                     (POTENTIAL).
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MEDLINE=5912852; PubMed=7827755;
BBLTY F. Neame P.J., Sasse J., Pearson D.;
"Length variation in the keratan sulfate domain of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 TEVLAYSNSSARGRAFLEHLTDL-----SIRGTLFVPQNSGLGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
          BY SIMILARITY.

N-LINKED (GLCNAC. .) (1

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N-LINKED (GLCNAC. .) (
                                                    N-LINKED (GLCNAC. .)
N-LINKED GLCNAC. .)
N-LINKED (GLCNAC. .)
                                                                                                                                                  Missing (in isoform 2) /FIId=VSP 003073. E -> D (\overline{IN} REF 3).
                                                                                                                                                                                 -> D (IN REF. 3)
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SIMILARITY
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Matrix Biol. 14:323-328(1994).
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                                                                                                                                                                                                             9.4%;
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                                                                                                                                                                                                                                    75; Conservative
                                                                                                                                                    1892
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330
388
439
644
700
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                                                                    CARBOHYD
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Best Local
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18. Biol. Chem. 268:17377-17383(1993).

19. Biol. Chem. 268:17377-17383(1993).

10. Biol. Chem. 268:17377-17383(1993).

21. FUNCTION: This proteoglycan is a major function of this protein is to resist compression in cartilage. It binds avidly to hardrance acid via an amino-terminal globular region. May play a regulatory role in the matrix assembly of the cartilage.

22. SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

23. DOMAIN: Two globular domains, Gl and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus. Gl contains link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B' motifie. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains, N-linked and O-linked oligosaccharides (By similarity).
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 4 link domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
                                                                                                                                Fueloep C., Walcz E., Valyon M., Glant T.T.;
"Expression of alternatively spliced epidermal growth factor-like
domains in aggrecans of different species. Evidence for a novel
                  Adams M.E., Kowk S.X.F., Huang D., Glant T.T., Fullop C., Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002353; AntifreezeII.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000742; EGF_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S74662; AAC60527.1; -.
EMBL; L07054; -; NOT_ANNOTATED_CDS
PIR; 146998; 146998.
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SMART; SW00034; CLECT; 1.
SMART; SW000179; BGF CA; 1.
SMART; SW00445; LINK; 4.
PROSITE; PS00010; ASX_HYDROXYL; 1.
                                                                                             TISSUE=Cartilage;
MEDLINE=93352525; PubMed=8349621;
SEQUENCE OF 1830-2333 FROM N.A.
                                                                           SEQUENCE OF 2082-2118 FROM N.A.
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EGF_like.
Ig_MHC.
Ig_MHC.
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Pfam; PF00193; Xlink; 4.
PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR01265; LINXMODULE.
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Pfam; PF00059; lectin_c; 1.
Pfam; PF02339; SGXXSG; 66.
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InterPro; IPR000436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| | :|||||:||:||:||
497 VFHYRPGSARYSLTFEEAQQACLRTGAVIASPEQLQAAYEAGYEQCDAGWLQDQTVRYPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557 VSPRTPCVGDKDSSPGVRTYGVRP-PSETYDVYCYVDK------LEGEVF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches 66; Indels 34; Gaps
                                                                                                                                     Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; EGF-like domain;
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GGLCNAC. .) (POTENTIAL).
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GGLCNAC. .) (POTENTIAL).
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GGLCNAC. .) (POTENTIAL).
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N-LINKED (GLCNAC. . .)
                                                                                                                                                                                   AGGRECAN CORE PROTEIN
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Pred. No. 6.7e-07;
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CS-1.
CS-2.
G3.
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747 74
2333 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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*** PAULINE-86250698; PubMed=2444893;

*** MEDLINE-86250698; PubMed=2444893;

*** NEDLINE-86250698; PubMed=2444893;

*** Deege K., Fernandez P., Hassell J.R., Sasaki M., Yamada Y.;

*** Partial cDNA sequence encoding a globular domain at the C terminus RT of the rat cartilage proteoglycan.";

*** Siol. Chem. 251:8108-8111(1986).

*** Is in Crem. 251:8108-8111(1986).

*** To fi the rat cartilage proteoglycan is a major component of extracellular matrix of cartilagenous tissues. A major function of this protein control of this protein control of this protein control of this protein control of the matrix assembly of the cartilage.

*** SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

*** SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

*** C -1- DOMAIN: Two globular domains. Gl and G2, comprise the amino consists of the proteoglycan, while another globular region, G3, makes up the COOM terminus. Gl contains link domains and thus consists of three disultide-bonded loop structures designated as the proteoglycan in the coom structures designated as the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the proteoglycan in the consists of the consists of the proteoglycan in the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the consists of the con
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-:- SIMILARITY: Contains 4 link domains.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
-:- SIMILARITY: Contains 1 Sushi (SCR) domain.
-:- SIMILARITY: Contains 1 Sushi (SCR) domain.
-:- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
                                                                                                              01-AUG-1988 (Rel. 08, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (CSPCP).
                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=88087070; PubMed=3693370;

MEDLINE=88087070; PubMed=3693370;

MEDGE K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.;

"Complete primary structure of the rat cartilage proteoglycan core procein deduced from cDNa clones.";

procein deduced from cDNa clones.";

J. Biol. Chem. 262:17757-17767(1987).
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Doege K., Sasaki M., Horigan E., Hassell J.R., Yamada Y.,
J. Biol. Chem. 263:10040-10040(1988).
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EMBL; J03485; AAA21000.1; ALT_SEQ.
PIR; A92623; A28452.
HSSP; P98066; 1TSG.
InterPro; IPR002353; Antifreezell.
InterPro; IPR007110; Ig-like.
InterPro; IPR03006; Ig_MHC.
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IPR001304;
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Bos taurus (Bovine).
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18.8%; Pred. No. 1.1e-06;
ve 24; Mismatches 65
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SWART; SM00046; CLECT; 1.
SWART; SM00406; IGV; 1.
SWART; SM00445; LINK; 4.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50941; C_TYPE_LECTIN_2; 1.
PROSITE; PS50935; IG_LIKE; 1.
PROSITE; PS00290; IG_MRC; 1.
PROSITE; PS01241; LINK; 4.
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InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00059; lectin c; 1.
Pfam; PF02339; SGXXSG; 55.
Pfam; PF00193; XIInk; 1.
Pfam; PF00193; XIInk; 4.
PRINTS; PR00336; ANTIFREZEII.
PRINTS; PR01265; LINKMODULE.
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FEBS Lett. 206:73-77(1986).

-!- FUNCTION: This proteoglycan is a major component of extracellular matrix of cartilagenous tissues. A major function of this protein is to resists compression in cartilage. It binds avidly to hyaluronic acid via an amino-terminal globular region. May play a regulatory role in the matrix assembly of the cartilage.
-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                 PGCA BOVIN STANDARD; PRT; 2364 AA.
P13608; P79117; Q28159;
01-JMV-1990 (Rel. 13, Created)
10-JMV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antonsson P., Heinegaard D., Oldberg A.;
"The keratan sulfate-enriched region of bovine cartilage proteoglycan consists of a consecutively repeated hexapeptide motif.";
J. Biol. Chem. 264:16170-16173(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perin J.-P., Bonnet F., Jolles J., Jolles P., "Sequence data concerning the protein core of the cartilage proteoglycan monomers. Characterization of a sequence allowing the synthesis of an oligomoleotide probe."; FEBS Lett. 176:37-42(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oldberg A., Antonsson P., Heinegaard D.; "The partial amino acid sequence of bovine cartilage proteoglycan, deduced from a cDNA clone, contains numerous Ser-Gly sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cartilage;

PUBDILNE=23552525; PubMed=8349621;

Fueloep C., Walcz E., Valyon M., Glant T.T.;

"Expression of alternatively spliced epidermal growth factor-like
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                                                                                 ------FATOMEQFTFQEAQAFCAAQNAT-LASTGQLYAAWSQGL 628
174 OVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Hering T.M., Kollar J., Huynh T.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 563-1056 FROM N.A.
MEDLINE=89380219; PubMed=2528543;
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MEDLINE=85027710; Pubmed=6489519;
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Biochem. J. 243:255-259(1987).
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ALTERNATIVE PRODUCTS:
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Name-1, Square-1, Square-e-Displayed,
Name-2, Principal Square-e-Wipe Dolo72,
CCC 1-DOMANN: Two globular domanne, Gland Globular region, Gl.
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Tand-e-Ferminas Gl. Constains Interface and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and that and the chondrolth nellete (ES) attachment domains lid between GZ and Gl. In the Santa School of the Contains I immunoglobulin-like V-type domain.

The Interpretation of the professy of the Contains I immunoglobulin-like V-type domain.

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
LINK 1.
LINK 2.
LINK 3.
LINK 4.
23 X 6 AA APPROXIMATE TANDEM REPEATS OF E-[EK]-P-P-P-S.
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Alternative splicing generates two different mRNA species for rat
link protein.".
J. Biol. Chem. 263:6063-6067(1988).
                                                                                                                                         EGF-LIKE, CALCIUM-BINDING (POTENTIAL)
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1-PEB-1996 (Rel. 33, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP)
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Doege K., Hassell J.R., Caterson B., Yamada Y.;
"Link protein cDNA sequence reveals a tandemly repeated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 9.1%; Score 170; DB 1; Length 2364; Local Similarity 38.9%; Pred. No. 1.5e-06; nes 37; Conservative 12; Mismatches 42; Indels 4
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RESULT 9
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HKIRIKTATSDY -> DCTAFWKLIRGRRESSAFVGIL
TMPCCFPWRKHYTWKGIKSLKLPSLAISDRTS (in
                                                                                                                                                                                                                                                              . Biol. Chem. 261:3519-3535(1986).

- FUNCTION: STABILIZE THE AGGREGATES OF PROTEOGLYCAN MONOMERS WITH HYALURONIC ACID IN THE EXTRACELLULAR CARTILAGE MATRIX.
                                                                                                                               MEDLINE=86140139; PubMed=2419334;
Neame P.J., Christner J.E., Baker J.R.;
"The primary structure of link protein from rat chondrosarcoma proteoglycan aggregate.";
J. Biol. Chem. 261:3519-3535(1986).
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-!- SIMILARITY: Contains 1 immunoglobulin-like_V-type domain.
-!- SIMILARITY: Contains 2 link domains.
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Missing (in isoform Short).
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PROTEOGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE.
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23278AEA56273D6C CRC64;
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                                   Proc. Natl. Acad. Sci. U.S.A. 83:3761-3765(1986).
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LINK 2.
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EMBL, M22335; AAA41535.1; JOINED.
EMBL, M22337; AAA41535.1; JOINED.
EMBL, M22339; AAA41535.1; JOINED.
EMBL, M22340; AAA41556.1; --
EMBL, M22340; AAA4156.1; JOINED.
EMBL, M22338; AAA41556.1; JOINED.
EMBL, M22338; AAA41536.1; JOINED.
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InterPro; IPR003596; Ig v.
InterPro; IPR000538; Link.
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354 AA;
                                                                                           SEQUENCE OF 16-354
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RC STRAIN-C57BL/G5. TISSUB-Embryo;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,

A.Zawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Yoshoo H., Kasukawa T., Saito R.,

RA Aizawa K., Isawa M., Ashburner M., Barlov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Barlov S., Casavant T.,

RA Achim D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suruki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suruki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

A Basaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

N Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havachiyaki V.,
                                                                                                                                                      167
                                                                                                      5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
                                                                                                                                                      ---EDDTAVVALELQGV---VFPYFPRL
                                                                                                                                                                                                 65 GOYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG
                                                                                                                                                                                                                            168 GRYNINFHEARQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCG
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-!- FUNCTION: Stabilizes the aggregates of proteoglycan monomers with
hyaluronic acid in the extracellular cartilage matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/Sv;
MEDLINE=20108790; PubMed=10640815;
Deak F., Mates L., Krysan K., Liu Z., Szabo P.E., Mann J.R.,
Beler D.R., Kiss I.,
"Characterization and chromosomal location of the mouse link protein
                                                       Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLK_MOUSE STANDARD; PRT; 356 AA.
Q9QUP5; Q9D1G9; Q9Z1X7;
L6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proceedlycan link protein precursor (Cartilage link protein) (LP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otto J.M., Cs-Szabo G., Kamath R.V., Liu W., Li Y., Glant T.T., "Molecular analysis of the murine link protein gene: 5' flanking, coding and 3' flanking sequence analysis, exon-intron structure; tissue distribution; and generation of transgenic mice."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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          Length 354;
                                                  52;
       9.1%; Score 169.5; DB 1; 10.8%; Pred. No. 1.5e-07;
Query Match
Best Local Similarity 30.8%; Pred. No. 1.5e-
                                                                                                                                                                                                                                                                                                125 --SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                             228 GONTVPGVRNÝGFWDKDKSRYDVFCF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytogenet. Cell Genet. 87:75-79(1999).
                                                                                                                                  |::|||
135 GRYKCE----VIEGL
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Local Similarity
                                                                          SEQUENCE FROM N.A.
                                                    NCBI_TaxID=9796;
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.5e-07;
20; Mismatches 52; Indels 29; Gaps
                                                                                                                                                                                                                               R InterPro; IPR007110; 19-like.
R InterPro; IPR007110; 19-like.
R InterPro; IPR003596; 1g_v.
R InterPro; IPR003596; 1g_v.
R InterPro; IPR0047; ig; 1.
R Pfam; PF00193; Xlink; 2.
R PENDOm; PD000919; LINKMODULE.
R PRNMT; SM00406; 1Gv; 1.
R SMART; SM00445; LINK; 2.
R PROSITE; PS50835; 1G LIKE; 1.
R PROSITE; PS01241; LINK; 2.
R PROSITE; PS01241; LINK; 2.
R Glycoprotein; Connective tissue; Extracellular matrix; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 356;
SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 2 link domains. SIMILARITY: STATEMENT SEQUENCE differs from that shown due to a frameshift in position 347.
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PROTEOGLYCAN LINK PROTEIN.
IG-LIKE V-TYPE.
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N-LINKED (GLORAC..
MISSING (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%; Score 169.5; 30.8%; Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 GONTVPGVRNYGFWDKDKSRYDVFCF 255
                                                                                                                                                                                           EMBL, AF098460; AAD12253.1; -.
EMBL, AKO05582; BAB22872.1; ALT_FRAME.
HSSP, P98066; ITSG.
MGD; MGI:1337006; Crtl1.
                                                                                                                                                                                                                                                                                                                                                                                                          LINK 1.
LINK 2.
                                                                                                                                     EMBL; AF137278; AAF24166.1; -.
EMBL; AF13775; AAF24166.1; JOINED.
EMBL; AF13776; AAF24166.1; JOINED.
EMBL; AF13727; AAF24166.1; JOINED.
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EMBL; AF098460; AAD12253.1;
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                                                                                                                                                                                                                                                                                                                                                                                         Am. J. Vet. Res. 56:959-965(1995).
-!- FUNCTION: Stabilizes the aggregates of proteoglycan monomers with
hyaluronic acid in the extracellular cartilage matrix (By
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                                                                                                                                                                                                                                                                                                  Dudhia J., Platt D.;
"Complete primary sequence of equine cartilage link protein deduced
from complementary DNA.";
Proteoglycan link protein precursor (Cartilage link protein) (LP).
                                                                      bydus cadailus (HOISE).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 link domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain; Repeat.
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PROTEOGLYCAN LINK PROTEIN.
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PROSITE; PS01241; LIÑK; 2.
Glycoprotein; Connective tissue; Extracellular matrix;
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LINK 2.
                                                                                                                                                                                                                                         TISSUE=Cartilage;
MEDLINE=96039874; PubMed=7574168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P98066; ITSG.
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig-v.
InterPro; IPR0005396; ig-v.
Pfam; PF00047; ig; 1.
Pfam; PF00193; xlink.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hyaluronic acid; Proteoglycan;
PROPEP 1 15 BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1265; LINKMODULE.
Probom; PD000918; Link; 2.
SMART; SM00406; IGV; 1.
SMART; SM00445; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.1%;
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                                                      Squus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S42938; S42938.
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                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20483618; PubMed=11027579;
Hirakawa S., Oohashi T., Su W.-D., Yoshioka H., Murakami T., Arata J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The brain link protein-1 (BRALI): cDNA cloning, genomic structure, and characterization as a novel link protein expressed in adult
                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             simlarity).
-!- TISGUE SPECIFICITY: Expressed only in adult brain.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 link domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 276:982-989(2000)
                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                         340 AA.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences.
                                                                                                                                                      Brain link protein-1 precursor
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                      BRA1 HUMAN
09GZV7;
                                                                                                                                                                                                                                                                                                                                                                                                                        Ninomiya Y.
BRA1_HUMAN
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BAB17669.1; JOINED. BAB17669.1; JOINED. BAB17669.1; JOINED.

EMBL; AB049061; BAB17669.1; -

AB049057; AB049058; AB049059;

EMBL; EMBL; EMBL; EMBL;

AB049060; BAB17669.1; JOINED. AB049054; BAB17662.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 IMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCGS-GVVGIVDYGPRPNKSEM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 RLATÝSÓLYQAWTEGLDWČNAGWLLEGSVRÝPVLTARAPČGGRĞRPGÍRSÝGPRDRMRDR 235
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"Bowine chondrocyte link protein cDNA sequence: interspecies
conservation of primary structure and mRNA untranslated regions.";
comp. Biochem. Physiol. 1128:197-203(1995).
-!- FUNCTION: Stabilizes the aggregates of proteoglycan monomers with
hyaluronic acid in the extracellular cartilage matrix.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 166; DB 1; Length 340;
31.7%; Pred. No. 2.9e-07;
iive 21; Mismatches 51; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                         SMART; SM00409; IG; 1.
SMART; SM00445; LINK; 2.
PROSITE; PSS0835; IG_LIXE; 1.
PROSITE; PSS01241; LINK; 1.
Proteoglycan; Hyaluronic acid; Extracellular matrix; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62CCC1D86385F5C7 CRC64;
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BRAIN LINK PROTEIN-1.
IG-LIKE V-TYPE.
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LINK 2.
BY SIMILARITY.
BY SIMILARITY.
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MEDLINE=96043243; PubMed=7584851;
                 PIR, JC7505; JC7505.
HSSP; P98066; ITSG.
InterPro; IPR00110; Ig-like.
InterPro; IPR00359; Ig.
InterPro; IPR00589; Ig.
Pfam; PF00047; ig; 1.
Pfam; PF00193; Xlink; 2.
EMBL; BC029864; AAH29864.1; -.
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ProDom; PD000918; Link; 2.
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170
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265
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340 AA;
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DISULFID
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DOMAIN
DOMAIN
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us-09-466-778b-11.rsp

Proc. Natl. Acad. Sci. U.S.A. 83:3766-3770(1986)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
     and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 GRYKCE----VIEGL-----VFPYFPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1988 (Rel. 07, Created)
1-APR-1988 (Rel. 07, Last sequence update)
15-WAR-2004 (Rel. 43, Last senotation update)
Proteoglycan link protein precursor (Cartilage link protein) (LP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete amino acid sequence of chicken cartilage link protein deduced from cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1265; LINKMODULE.
Probom; PRO00918; Link; 2.
SMART; SMO0445; LINK; 2.
PROSTIE; PSS0835; LG LIKE; 1.
PROSTIE; PSS01241; LINK; 2.
Glycoprotein; Connective tissue; Extracellular matrix;
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
1 15 PROFED
CHAIN
16 354 PROTEOGLYCAN LINK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%; Score 165.5; DB 1; Length 354; 30.1%; Pred. No. 3.4e-07; Live 22; Mismatches 51; Indels 29
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TISSUB=Embryonic sternal cartilage;
TISSUB=Embryonic sternal cartilage;

Deak F. Kiss I., Sparks K.J., Argraves W.S., Hampikian G., Goetinck P.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    065D155378A1283C CRC64;
between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There as
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 GONTVPGVRNÝGFWDKDKSRYDVFCF 253
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LINK 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40287 MW;
                                                                                                                                                                                                                                HSSP; P98066; 1TSG.
InterPro; IPR007110; Ig-like.
InterPro; IPR005596; Ig v
InterPro; IPR000538; Link.
                                                                                                                                                                                                        EMBL; U02292; AAC04311.1; -.
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                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; i.
Pfam; PF00193; Xlink; 2.
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253
350
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Matches 44; Conserv
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P07354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                            MEDLINE-87317659; PubMed=3476955;
Kibs I., Deak F., Mestric S., Dellus H., Soos J., Dekany K.,
Aggraves W.S., Sparks K.J., Goetinck P.F.;
"Structure of the chicken link protein gene: exons correlate with the
                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 84:6399-6403(1987).
-!- FUNCTION: Stabilizes the aggregates of proteoglycan monomers with hyaluronic acid in the extracellular cartilage matrix.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 link domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSP-
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N-LINKED (GLOMAC. ..) (POTENTIAL).
N-LINKED (GLOMAC. ..) (POTENTIAL).
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Hyaluronic acid; Proteoglycan; Immunoglobulin domain; Repeat.
PROPEP 1 9
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2581CAE22158B60F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 29.9%; Pred. No. 3.4e-07, 44; Conservative 26; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE V-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 G--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 GGKNTVPGVRNYGFWDKERSRYDVFCF 254
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                                                                                                                                                                                                                                                                                                                                                         EMBL, M35038; AAA48941.1; -
EMBL, M35035, AAA48941.1; JOINED.
EMBL; M35036, AAA48941.1; JOINED.
EMBL; M35037; AAA48941.1; JOINED.
EMBL, M35037; AAA48940.1; -
PIR, A28305; LKCH.
HSSP, P98066; 1TSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40533 MW;
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InterPro; IPR003596; Ig v.
InterPro; IPR000538; Link.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 1. PROSITE; PS01241; LINK; 2.
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ProDom; PD000918; Link; 2.
SMART; SM00406; IGV; 1.
SMART; SM00445; LINK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1.
Pfam; PF00193; Xlink; 2.
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21
56
355 AA;
                                                                                                            protein domains.";
                              SEQUENCE FROM N.A.
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                   or send an email to license@isb-sib.ch).
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LINK 4.
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InterPro; IPR003324; SGXXSG.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G1-B'.
G2-B.
G2-B'.
                                                                                                                                            MGD; MGI:99602; Agci.
InterPro; IPR002353; Antifreezell.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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                                                                         EMBL, S73722; AAB32160.1; -.
EMBL; S73721, AAB32160.1; JOINED.
PIR; A55182; A55182.
HSSP, P98066; 1TSG.
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00059; lectin_c; 1.
Pfam; PF02339; SGXXSG; 60.
Pfam; PF00193; Rushi; 1.
Pfam; PF00193; Xlink; 4.
PRINTS; PR00135; AWTIFREEZEII.
PRINTS; PR01265; LINKMODULE.
                                                                                                                                                                                                                         IPR003596; Ig_v.
IPR001304; Lectin_C.
                                                     EMBL; L07049; AAC37670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom, PD000918; Link; 4.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00406; IGY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Link; 4.
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1917
2132
133
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SIGNAL
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: Contains mostly chondroitin sulfate, but also keratan sulfate chains, N-linked and O-linked oligosaccharides.
-!- DISEASE: Defects in AGC1 are the cause of cartilage matrix deficiency (CMD). CMD is an autosomal recessive syndrome characterized by cleft palate, short limbs, tail and snout.

Mutation in strain CMD causes absence of aggrecan by truncation of the protein (mutation in the Gl domain).
-!- SIMILARITY: Contains 4 link domains.
-!- SIMILARITY: Contains 1 limmunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 1 sush (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).

DOMAIN: Two globular domains, Gl and G2, comprise the amino terminus of the proteoglycan, while another globular region, G3, makes up the COOH terminus link domains and thus consists of three disulfide-bonded loop structures designated as the A, B, B' motifs. G2 is similar to G1. The keratan sulfate (KS) and the chondroitin sulfate (CS) attachment domains lie between G2
                             PGCA MOUSE STANDARD; PRT; 2132 AA.

061282; 064021;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 31, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aggrecan core protein precursor (Cartilage-specific proteoglycan core protein) (GSPCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: This proteoglycan is a major component of extracellular FUNCTION: This proteoglycan is a major component of this protein is to resist compression in cartilage. It binds avidly to hyaluronic acid via an amino-terminal globular region. May play a subsulvir: Interacts with FBLM1.

SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada Y.;
"Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99329059; PubMed=10400671;
Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
"Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
                                                                                                                                                                                                                                                                                              STRAIN=BALB/c; TISSUE=Cartilage;
MEDINE=59104847; PubMed=7866222;
Waloz E., Deak F., Ethardt P., Coulter S.N., Fueloep C., Horvath P.,
Doege K.J., Glant T.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe H., Kimata K., Line S., Strong D., Gao L.-Y., Kozak C.A.,
                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                           "Complete coding sequence, deduced primary structure, chromosomal localization, and structural analysis of murine aggrecan."; Genomics 22:364-371(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95004579; PubMed=7920633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 211-326 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the aggrecan gene.";
Nat. Genet. 7:154-157(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH FBLN1.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129/Sv;
                                                                                                                                                                   AGC1 OR AGC
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(POTENTIAL).
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PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
PROSITE; PS50050; IG_MRE; 1.
PROSITE; PS00200; IG_MRC; 1.
PROSITE; PS01241; LINK; 4.
Glycoprotein; Proteoglycan; Lectin; Signal; Sushi; Repeat;
                                                                                                                                                                                                                                                           POTENTIAL.
AGGRECAN CORE PROTEIN.
IG-LIKE V-TYPE.
                                                                                                                                                                                                                                                                                                                                                          KS.
CS-1.
CS-2.
G3-3.
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us-09-466-778b-11.rsp

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MEDLINE=21676785; PubMed=11817897;

Mohashi T., Hirakawa S., Bekku Y., Rauch U., Zimmermann D.R.,

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

Su W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Y.;

W.-D., Ohtsuka A., Murakami T., Ninomiya Mich House System (CNS) Which facilitates neuronal conduction and general structural stabilization. Binds to hyaluronic acid.

Submittates neuronal conduction and general structural stabilization. Binds to hyaluronic acid.

T. SUBGELULAR LOCATION: Secreted; extracellular matrix.

Colocalizes with versican V2 in decoloping and adult cerebellar which where matter and at the nodes of ranvier.

C. I. DEVELOPMENTAL STAGE: Expression starts at postnatal day 20 and
                                                                                                                                                                                                     57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                       547
                                                                                                                                                                                                                                                                                             117 AFASONC --- GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLL 173
                                                                                                                                                                                                                                              488 VFHYRPGSTRYSLTFEEAQQACMHTGALIASPEQLQAAYEAGYEQCDAGWLQDQTVRYPI
                                                                                                                                                                                                                                                                                                                            548 VSPRTPCVGDKDSSPGVRTYRVRPS-SETYDVYCYVDK-----LEGEVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20483618; PubMed=11027579;
Hirakawa S., Oohashi T., Su W.-D., Yoshioka H., Murakami T., Arata J.,
                                                                                                                                                             66; Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The brain link protein-1 (BRALI): cDNA cloning, genomic structure, and characterization as a novel link protein expressed in adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
667 667 N-LINKED (GLCNAC. .) (POTENTIAL).
1675 1675 N-LINKED (GLCNAC. .) (POTENTIAL).
1171 1173 CELL ATTACHMENT SITE (POTENTIAL).
2132 AA; 222008 MW; 0B2BCDFC6CBDA163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     174 OVLMSFPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                591 ------FATRLEQFTFQEARAFCAAQNAT-LASTGQLYAAWSQGL 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 2 link domains.
                                                                                                                  Length 2132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 276:982-989 (2000)
                                                                                                             / Match 8.8%; Score 165; DB 1; Local Similarity 28.8%; Pred. No. 3.7e-06; Nes 49; Conservative 23; Mismatches 66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AA
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  CARBOHYD
                                                                  SEQUENCE
                                                                                                             Query Match
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Q9ESM3;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 RLATYGQLYQAWTEGLDWCNAGWLLEGSVRYPVLTARAPCGGHGRPGIRSYGPRDRSRDR 236
                                                                                                                                                                                                                                                                                                                                                                                                               33 LQDNGQCHADAKÇVDLH-FQDTTVG-----VFHLRSPLGQYKLTFDKAREACANEAA 83
                                                                                                                                                 SMART; SM00406; IGV; 1.
SMART; SM00445; LINK; 2.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS01241; LINK; 2.
Proteoglycan; Hyaluronic acid; Extracellular matrix; Signal;
                                                                                                                                                                                                                                                                                                                                                                 Length 341;
                                                                                                                                                                                                                                                                                                                                          1F65DCD07B5CFF02 CRC64;
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BRAIN LINK PROTEIN-1.
IG-LIKE V-TYPE.
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11.7%; Pred. No. 4.4e-07;
.ve 19; Mismatches 53;
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            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           LINK 1.
LINK 2.
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                                                      MGD; MGI:2131300; Brall.
InterPro; IPR007110; Ig-like.
InterPro; IPR005196; Ig_v.
InterPro; IPR005396; Link.
Pfam; PF00193; Xlink; Z.
PRINTS; PR01265; LINKWODULE.
ProDom; PD000918; Link; Z.
                                  EMBL; AB049055; BAB17663.1; -.
                                                                                                                                                                                                                                                                                                                                          37925 MW;
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341 AA;
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                                              HSSP; P98066; 1TSG.
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52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 277 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
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US-08-024-868-2
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1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353
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1: /cgr2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUG COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUG COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-242-097-2
US-09-206-695-2
US-09-709-118-2
US-09-907-794A-213
US-09-907-794A-213
US-09-907-75A-213
US-09-905-125A-213
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PCT-US95-04353-6
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US-09-206-695-4
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US-08-225-477B-8
PCT-US95-04353-8
US-08-340-428B-49
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PCT-US95-04353-3
US-08-225-4778-4
PCT-US95-04353-4
PCT-US95-03747-2
US-09-010-1478-20
US-08-22-097-5
US-09-206-695-5
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Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Sequence 5, Appli Sequence 3, Appli Sequence 9, Appli Sequence 9, Appli Sequence 21, Appl Sequence 21, Appl Sequence 201, App Sequence 201, App Sequence 201, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl		of DNA
PCT-US95-04353-5 5180808-2 9CT-US95-03747-3 US-08-225-4477B-9 PCT-US95-04353-9 US-09-232-160-21 US-09-907-794A-201 US-09-907-794A-201 US-09-905-125A-201 US-09-905-125A-201 US-09-822-880-2 US-09-820-170A-34 US-09-273-565-34 US-09-273-565-34 US-09-273-565-34 US-09-273-565-34 US-09-273-565-34 US-09-273-565-34 US-09-273-565-34 US-09-661-468-34 US-09-976-165-34	AL I GNMENTS	US/08024868 Ho i, Hans Georg an Cytckine-Induced Protein, TSG-6 Coding Therefor and Uses Thereo S: and Neimark h Street, NW PC-DOS/MS-DOS PC-DOS/MS-DOS Release #1.24 NATA: US/08/024,868 5 A: US/08/024,868 5 A: US/08/024,868 5 A: US/08/024,868 1: 33,949 MMBER: VILCEK=1 ORMATION: 1: 13,949 MMBER: VILCEK=1 ORMATION: 1:-13197 1:-5197
1.1 2432 29 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		ion : : :
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APPLICANT: Lee, Tae Ho
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Oxtokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                   Sequence 2, Application US/08242097
Patent No. 5846763
GENERAL INFORMATION
APPLICANT: Lee, Tae Ho
APPLICANT: Wieniewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF SEQUENCES: 11
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                                                                          112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BEGINSTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6210905
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TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 43.3%
Matches 45; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Browdy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
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A Pharmaceutical Composition
Containing TSG-6 Protein for Treating Inflammatory Diseases and
Cancer-Related Pathologies and Methods of Using same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,179 FILING DATE:
                                                                         STATE: D.C.
ZIP: 20004

COMPUTER FEADMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 262; DB 3; ilarity 43.3%; Pred. No. 4.1e-20; Conservative 16; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Browdy and Neimark
STREE: 419 Seventh Street, N.W., Suite 300
STATE: Washington
STATE: D.C.
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEE26/VILCEK=1B
                                                                                                                                                                                                                                                                                      AFFLICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09000179
Patent No. 6313091
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/24 FILING DATE: 13-MAY-1994 ATTORNEY/AGENT INFORMATION: NAME: BROWDY, ROGER I. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 277 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A PITTLE OF INVENTION: CONTITLE OF INVENTION: CANNUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-206-695-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20004
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 45; Conserv
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LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                               43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGGE L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B
TELECOWUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,118
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
                                                              REFERENCE COURSEN. 20,010
REFERENCE CONTROL OF TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEPHONE: 212-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lee, Tae Ho
Wisniewski, Hans Georg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09799118
Patent No. 6518401
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 277 amino acids TYPE: amino acid
                                    NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                           LANGTH: 277 amino acids
TYPE: amino acid
TYPE: amino acid
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            ATTORNEY/AGENT INFORMATION: NAME: BROWDY, ROGER L.
20-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                 45; Conservative
                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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Best Local Similarity
FILING DATE:
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US-09-799-118-2
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A Pharmaceutical Composition Containing TSG-6
Protein for Treating Inflammatory Diseases and Cancer-Related 1
Methods of Using same
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                                                                                                                                          32 ERAAGVYHREARSGKYKLIYAEAKAVCEFEGGHLAIYKQLEAARKIGFHVCAAGWMAKGR 91
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     Length 277;
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                                                                                                                                                                                            112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
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                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUREBUT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11995
                                                    43;
Query Match
Best Local Similarity 43.3%; Pred. No. 4.1e-20;
Matches 45; Conservative 16; Mismatches 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.0%; Score 262; DB 5;
Best Local Similarity 43.3%; Pred. No. 4.1e-20;
Matches 45; Conservative 16; Mismatches 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,311
FILING DATE: 20-UUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 213, Application US/09907794A; Patent No. 6635468
                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application PC/TUS9611995 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WISN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25,618
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 277 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A PHITLE OF INVENTION: PROTITLE OF INVENTION: MethNUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein PCT-US96-11995-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abba.
STREET: 419 sc.
CITY: Washington
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CLASSIFICATION:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
IIITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IIITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1200-02-22
PRIOR FILING DATE: 1399-07-07
PRIOR FILING DATE: 1399-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1399-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1399-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING DATE: 2001-07-17
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 213
LENGTH: 360
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FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
APPLICATION NUMBER: PCT/US99/28313
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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FILING DATE: 1999-09-15
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FILING DATE: 1999-12-02
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FILING DATE: 1999-12-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US99/30095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                Gurney, Austin L.
Hillan, Kenneth, J.
                                                                                                                        errara, Napoleone
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                   Gerritsen, Mary E.
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Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1999-09-13
                                                                                                                                                                                                     Gao, Wei-Qiang
Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1999-09-15
Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                            ong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-09-907-794A-213
                                                                                                                                                                                                                                                                             Goddard, A.
                                                                          APPLICANT
                                                                                                      PPLICANT
                                                                                                                                                       PPLICANT
                                                     APPLICANT
                                                                                                                                                                                                                            APPLICANT
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DB 4; Length 360;

10.1%; Score 187.5;

Query Match

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                                                                                                                                                                                      65 GQYKLIFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
                              29; Gaps
                           48; Indels
     30.8%; Pred. No. 8.1e-12;
ive 24; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR AFFLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-07
PRIOR PLILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
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; Sequence 213, Application US/09905125A
; Patent No. 6664376
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Grimaldi, Christopher J.
Gurney, Austin L.
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Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                 142 GRYRCE----VIDGLEDE-
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Filvaroff, Ellen
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Botstein, David
Best Local Similarity 30.8
Matches 45; Conservative
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Eaton, Dan L.
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PRILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 213
LENGTH: 360
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CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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Grimaldi, Christopher J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Betsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT:
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65 GOYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASGNCG 124
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Patent No. 5635370
SENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Protein
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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CITY: Stamford
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                      PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
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PRIOR PILING DATE: 1999-09-15
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APPLICATION NUMBER: US 60/143,048
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Matches 45; Conserv
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us-09-466-778b-11.rai

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NAME/KEY: rat link protein
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225
FILING DATE: April 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 residues
    SYSTEM: MS DOS
Word Processor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 31.5%
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                              LENGTH: 326 residues
TYPE: amino acid
STRANDEDNESS: single
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STREET: 419 cc.
CITY. Washington
STATE: D.C.
71P: 20004
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DATE: 1986
                                                                                    FILING DATE:
                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 9.0%; Score 167; DB 1; Length 326; l Similarity 31.5%; Pred. No. 1.2e-09; 46; Conservative 21; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: St. Onge Steward Johnston & Reens STREET: 986 Bedford Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: Doege, K., Hassell, J.R., Ca-AUTHORS: terson, B., and Yamada, Y.
TITLE: Link protein cDNA sequence reveals a
TITLE: tandemly repeated protein sequence.
JOURNAL: Proc. Natl. Acad. Sci. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application PC/TUS9504353
GENERAL INFORMATION:
APPLICANT: Susan Hockfield
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: 1BM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,477B
FILING DATE: April 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 GONTVPGVRNYG-FWDKDSRYDVFCF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                        1751-P0004
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MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: polypeptide FRAGMENT TYPE: functional domains
                                                                                                                                                                            NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REFRENCE/DOCKET NUMBER: 1751
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEFAK: 203-327-1096
                                                                                                                                                                                                                                                                       TELEFAX: 203-327-1050
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 326 residues
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: rat link protein
PUBLICATION INFORMATION:
AUTHORS: Doege, K., Hassell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VOLUME: 83
PAGES: 3761-3765
DATE: 1986
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Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GRYNLNFHEARQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Indels 30; Gaps
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%; Score 167; DB 5; Length 326; 31.5%; Pred. No. 1.2e-09; tive 21; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Doege, K., Hassell, J.R., Ca-AUTHORS: terson, B., and Yamada, Y.
TITLE: Link protein CDNa sequence reveals a
TITLE: tandemly repeated protein sequence.
JOURNAL: Proc. Natl. Acad. Sci. USA
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                                                                                                                                                                                                                                                                     1751-P0004
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
DESCRIPTION: polypeptide
FRAGMENT TYPE: functional domains
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Patent No. 5846763
GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Wieniewski, Hans Georg
APPLICANT: Vilcek, Jan
                                                                                                                      08/225,477
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| SEYKCE----VIEGL-----
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                                                                                                                                                                                                         NAME: Mary M. Krinsky
REGISTRATION NUMBER: 32423
REPERENCE/DOCKET NUMBER: 1751
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEFAX: 203-327-1096
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SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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                        98 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
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US-09-206-695-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lee, Tae Ho
APPLICANT: Wishiewski, Hans Georg
APPLICANT: Wishiewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.6%; Score 160; DB 2; Length 98; 36.2%; Pred. No. 1.1e-09; tive 17; Mismatches 41; Indels
                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AFASONCG--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 TKPREPCGGQNTVPGVRNYGFWDKDKSRYDVPCF 96
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                                                                                                                                                                                         25,618
FR: LEE26/VILCEK=1B
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APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                              APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/206,695
                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09206695 Patent No. 6210905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Browdy and Neimark
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BROWNY, ROGET L.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: LEEZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEPHONE: 212-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,618
  IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CILL.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
TELEFAX: 2
  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-242-097-4
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US-09-206-695-4
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57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
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                                                                                                                                                    3 VFPYFPRLGRYNLNFHEARQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPI 62
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
Therefor and Uses Thereof
                                                               .,
Query Match 8.6%; Score 160; DB 3; Length 98; Best Local Similarity 36.2%; Pred. No. 1.1e-09; Matches 34; Conservative 17; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.6%; Score 160; DB 4; Length 98; Best Local Similarity 36.2%; Pred. No. 1.1e-09; Matches 34; Conservative 17; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LEE26/VILCEK=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-628-5197
TELEPHONE: 212-737-3528
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                117 AFASONCG--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                          63 TKPREPCGGONTVPGVRNYGFWDKDKSRYDVFCF 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,118
FILING DATE: 06-Mar-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/242,097
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wisniewski, Hans Georg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09799118
Patent No. 6518401
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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Job time : 24 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ODTIVGVFHLRSPLGQYKLIFDKAREACANEAAIWATYNQLSYXQKAKYHLCSAGWLETG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NGQCHADAKCVDLHF 50
3 VFPYFPRLGRYNLNFHEARQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 37; Gaps
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8.4%; Score 157.5; DB 1; Length 371;
Best Local Similarity 27.9%; Pred. No. 1.6e-08;
Matches 46; Conservative 22; Mismatches 60; Indels 37.
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(THER INFORMATION: polypeptide encod-
) CTHER INFORMATION: ed by (and set out under) SEQ ID NO 1
US-08-225-477B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 RVAYPTAFASQNCGSGVVGIVDYGPRPN-----KSEMWDVFCYR 149
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                                                                                                                                                                                     Sequence 8, Application US/08225477B
Patent No. 5635370
GENERAL INFORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BERAB, A Brain Hya-
TITLE OF INVENTION: LICONARIA OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge Steward Johnston & Reens
STREET: 986 Bedford Street
CITY: Stamford
                                           117 AFASQNCG--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                       63 TKPREPCGGONTVPGVRNYGFWDKDKSRYDVFCF 96
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APPLICATION NUMBER: US/08/225,477B
FILING DATE: April 8, 1994
ATTORNEY,AGENT INFORMATION:
NAME: MALY M. KRINSKY
REGISTRATION NUMBER: 32423
REBERENCH DOCKET NUMBER: 1751-P0004
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECOMONICATION SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acids
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
2IP: 06905
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
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DESCRIPTION: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: en
IMMEDIATE SOURCE:
                                                                                                                                                                              US-08-225-477B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: S
STATE:
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March 30, 2004, 15:42:36; Search time 45 Seconds (without alignments) 2052.591 Million cell updates/sec 1865 1 MTGPGKHKCECKSHYVGDGL......ALAAYSYFRINRKTIGFXHF 353 Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:* GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 1065169 seqs, 261661801 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries - protein search, using sw model Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-09-466-778B-11 **BLOSUM62** Title: Perfect score: Scoring table: OM protein Database : Sequence: Searched: Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 40, Appl	Sequence 40, Appl	Sequence 25, Appl	Sequence 4, Appli	Sequence 20, Appl	Sequence 41, Appl	211,	٠,	Sequence 211, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 39, Appl	Sequence 39, Appl
	ID	US-10-028-248A-40	US-10-107-782-40	US-09-842-930A-25	US-10-133-172-4	US-10-133-172-20	US-10-028-248A-41	US-10-028-248A-211	US-10-107-782-41	US-10-107-782-211	US-10-028-248A-2	US-10-107-782-2	US-09-842-930A-2	US-10-133-172-2	US-10-028-248A-39	US-10-107-782-39
	DB	15	15	g)	14	14	15	15	15	15	15	15	σ	14	15	15
	ength	1192	1192	1394				897		897					1069	
æ (Query Match Length DB	95.0	95.0	95.0	95.0	95.0	94.9	94.9	94.9	94.9	83.3	83.3	81.2	81.2	79.4	79.4
	Score	1772	1772	1772	1772	1772	1769	1769	1769	1769	1554	1554	1514.5	1514.5	1480	1480
	No.	7	7	m	4	5	9	7	80	6	10	11	12	13	14	. 15

444	272	44	108	110, 2	3794,	Sequence 2580, Ap Sequence 5. Appli	\sim	g)	292,	Sequence 1237, Ap	294,	82,	46,	46,	213,	213,	213,	213,		213,	e 213	213	N
US-10-028-248 US-10-107-782 US-10-028-248	10-107-782-4 10-264-237-2	US-10-028-248A- US-10-107-782-4	0 US-09-774-639-108 0 US-09-969-730-110	US-10-621-363	-104-047-3	5 US-IU-IU4-047-2580 4 US-I0-133-172-5	9-118	4 US-10-247-671-185	5 US-10-295-027-292	5 US-10-295-027-1237			5 US-10-028-248A-46	5 US-1:0-107-782-46	US-09-909-320-213	S	US-09-905-291A-213	US-09-902-853-213	US-09-907-824-213	US-09-907-841-213	-60	OS-09-	0 US-09-906-838-213
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847 847 668	661.5	652.5	645.5	645.5	642	505	262	262	262	262	244	213	196	196	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5	187.5
16 17 18	13 20 21 21 21	7.7 7.7 7.7	23	25	56	7 7 7 7 8 7 7 8 9 7 9 9 9 9 9 9 9 9 9 9	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

APPLICANT: Rothenberg, Mark TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods TITLE OF INVENTION: Thereof FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256619
PRIOR FILING DATE: 2000-12-19
PRIOR PELLING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/262959
PRIOR FILING DATE: 2001-01-19 Sequence 40, Application US/10028248A Publication No. US20030235882A1 GENERAL INFORMATION: Patturajan, Meera Vernet, Corine Caman, Stacie Malyankar, Uriel Shenoy, Suresh Spytek, Kimberly Gangolli, Esha Miller, Charles Boldog, Ferenc Li, Li Taupier Ur, Raymond J Smithson, Glennda Zerhusen, Bryan Tchernev, Velizar Si, Jingsheng Edinger, Shlomit Stone, David Sciore, Paul Millet, Isabelle APPLICANT: Shimkets, Richard Colman, Steven Liu, Xiaohong US-10-028-248A-40 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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964 SLINFLIEVLAYSNSSARGRAFLEHLIDLSIRGILFVPQNSGLGENETLSGRDIEHHLAN 1023
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                                                                                                                                                                                                                                                                                                           DB 15; Length 1192;
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Pred. No. 1.5e-183;
2; Mismatches 17;
PRIOR APPLICATION NUMBER: 60/272408
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-20
PRIOR PRIOR APPLICATION NUMBER: 60/308039
PRIOR PELING DATE: 2001-07-26
PRIOR PILING DATE: 2001-07-26
PRIOR PILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 211
SEQ ID NO 40
LENGTH: 1192
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Io. US20040018970A1
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Spytek, Kimberly,
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Vernet, Corine,
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Malyankar, Uriel,
Miller, Charles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shenoy, Suresh,
Shimkets, Richard,
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Rothenberg, Mark,
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Gangolli, Esha,
Kekuda, Ramesh,
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Matches 334; Conservative
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Colman, Steve,
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Stone, David,
                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-028-248A-40
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Publication No.
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Best Local
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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1024 VSMFFYNDLVNGTTLQTRLGSKLLITASQDFLQPTETRFVDGRAILQWDIFASNGIIHVI 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             844 RSPLGQYKLTFDKAREACANEAATWATYNQLSYAQKAKYHICSAGWLETGRVAYPTAFAS 903
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TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
FILE REFERENCE: 5820.603
CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
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                                                                                                                                       CUCKERN FILING DATE: 2002-03-2/
PRIOR FILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/26,959
PRIOR PELING DATE: 2001-01-19
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-02-28
PRIOR PELING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/308,039
PRIOR PILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311,266
PRIOR PILING DATE: 2001-07-26
PRIOR PELING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
PRIOR PELING DATE: 2001-03-28
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Best Local Similarity
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US-09-842-930A-25
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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US-10-133-172-20
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Best Local Similarity
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TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FILE REFERENCE: 5864.014
CURRENT PRILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/286,468
PRIOR APPLICATION NUMBER: 00/286,468
PRIOR PLILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 09/842,930
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEC ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1416
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                                                                                                                                      95.0%; Score 1772; DB 9; Length 1394; 94.6%; Pred. No. 1.9e-183; tive 2; Mismatches 17; Indels 0
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SOFTWARE: Patentin version 3.1
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                                                                             ORGANISM: Homo sapiens
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US-10-133-172-4
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APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
FILE REPERENCE: 5864.014
CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/286,468
PRIOR APPLICATION NUMBER: 09/842,930
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
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Sequence 20. Application US/10133172
Publication No. US20030104987A1
SENERAL INFORMATION:
APPLICANT: WEIGEL, PAUL H
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APPLICANT: Sciore, Paul
APPLICANT: Milet, Isabelle
APPLICANT: Milet, Isabelle
APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods of
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
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  789 SRPLKAPPADVILHHTGLGAGIFFAIILVTGAVALAAYSYFRINRRTIGFQHF 841
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PRIOR FILING DATE: 2001-01-19
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/285189
PRIOR APPLICATION NUMBER: 60/308039
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
PRIOR SEQ ID NOS: 210
NUMBER OF SEQ ID NOS: 21
                                                                                                                                   Sequence 211, Application US/10028248A Publication No. US20030235882A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/256619
PRIOR FILING DATE: 2000-12-19
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Vernet, Corine
Casman, Stacie
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Shenoy, Suresh
Spytek, Kimberly
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Miller, Charles
Boldog, Ferenc
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Edinger, Shlomit
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CRGANISM: Homo sapiens
US-10-028-248A-211
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TITLE OF INVENTION: No. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
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PRIOR APPLICATION NUMBER: 60/25619
PRIOR PLING DATE: 2000-12-19
PRIOR PLING DATE: 2000-12-19
PRIOR PPLING DATE: 2001-01-19
PRIOR PPLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272408
PRIOR APPLICATION NUMBER: 60/285189
PRIOR PILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR PLING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 60/301266
PRIOR FILING DATE: 2001-08-09
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Kekuda, Ramesh
Patturajan, Meera
Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
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Zerhusen, Bryan
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Edinger, Shlomit
Stone, David
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Millet, Isabelle
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Miller, Charles
Boldog, Ferenc
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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APPLICANT: Zerhusen, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 21402-222CIP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT FILING DATE: 2002-03-27
                                                                                         548
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                                                                                         489 MIGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                      61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS
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                                           1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
  Gaps
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  17; Indels
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/256, 619
PRIOR APPLICATION NUMBER: 60/262, 959
PRIOR APPLICATION NUMBER: 60/262, 959
PRIOR PILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272, 408
PRIOR APPLICATION NUMBER: 60/272, 408
PRIOR APPLICATION NUMBER: 60/285, 189
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-04-20
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PRIOR APPLICATION NUMBER: 60/308,039
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Publication No. US20040018970A1
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PRIOR APPLICATION NUMBER: 60/311,266
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Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Colman, Steve,
Edinger, Shlomit,
Gangolli, Esha,
Kekuda, Ramesh,
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Vernet, Corine,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
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Rothenberg, Mark,
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  Conservative
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Matches 333;
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REPRENCE: 21402-22CTP
CURRENT APPLICATION NUMBER: US/10/107,782
CURRENT PILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 10/28,248
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR APPLICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-02-18
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-03-28
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PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-28
PRIOR PILING DATE: 2001-03-28
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                        181 SLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 240
                                                  729 VSMFFYNDLVNGTTLQTRVGSKLLITASQDPLQPTETRFVDGRAILQMDIFASNGIIHVI
                                                                                                            241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI
                                                                                                                                                                                                       301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
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PRIOR FILIND DATE: 2001-03-28
WIMBER OF SEQ ID NOS: 215
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application US/10107782
Publication No US20040018970A1
GENERAL INFORMATION:
APPLICANT: Boldog, Ferenc,
APPLICANT: Casman, Steate
APPLICANT: Colman, Steve,
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Tchernev, Velizar,
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Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Rothenberg, Mark,
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Gangolli, Esha,
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Malyankar, Uriel,
Miller, Charles,
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CRGANISM: Homo sapiens
US-10-107-782-41
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Best Local Similarity
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LENGTH: 897
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PRIOR APPLICATION NUMBER: 60/25619
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2001-01-19
PRIOR PLING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/272408
PRIOR APPLICATION NUMBER: 60/285189
PRIOR APPLICATION NUMBER: 60/386189
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR FILING DATE: 2001-04-20
PRIOR SPELICATION NUMBER: 60/311266
PRIOR APPLICATION NUMBER: 60/311266
PRIOR SEC ID NOS: 211
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 CURRENT FILING DATE: 2001-12-19
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Colman, Steve,
Edinger, Shlomit,
Gangolli, Esha,
Kekuda, Ramesh,
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Liu, Xiaohong,
Malyankar, Uriel,
Miller, Charles,
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                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                  2675
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APPLICANT:
APPLICANT:
APPLICANT:
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LENGIH: 26
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APPLICANT: Rothenberg, Mark
TITLE OF INVENTION: NO. US20030235882Alel Nucleic Acids and Polypeptides and Methods
TITLE OF INVENTION: Thereof
FILE REFERENCE: 21402-222
CURRENT APPLICATION NUMBER: US/10/028,248A
                                                                                                                                                                                                                                                                                                            489 MTGPGKHKCECKSHYVGDGLNCEPEQLFIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 548
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PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION UNDBER: 60/279,344
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 215
SOFTWARE: CHRASeqList Version 0.1
SEQ ID NO 211
LENGTH: 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10028248A Publication No. US20030235882A1 GENERAL INFORMATION:
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Taupier Jr, Raymond J
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Vernet, Corine
Casman, Stacie
Malyankar, Uriel
Shenoy, Suresh
Spytek, Kimberly
Gangolli, Esha
Miller, Charles
Boldog, Ferenc
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Tchernev, Velizar
Si, Jingsheng
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Zerhueen, Bryan
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Sciore, Paul
Millet, Isabelle
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                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-782-211
                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                         Matches 333;
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Best Local 8
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APPLICANT:
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2303 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 2362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2454 -----EVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLLQVLMSFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SITNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2507 VSMFFYNDLVNGTTLQTRLGSKLLITASQDPLQPVQSRFVDGRAILQWDIFASNGIIHVI
                                                                                                                                                                                                                                                                                                                                                         Query Match 83.3%; Score 1554; DB 15; Length 2675; Best Local Similarity 83.9%; Pred. No. 3.1e-159; Matches 296; Conservative 5; Mismatches 16; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                          NAME/KEY: UNSURE: LOCATION: (427)...(428)
COTHER INFORMATION: Wherein Xaa is any naturally occurring amino acid
US-10-028-2488-2
LOCATION: (55)..(56)
OTHER INFORMATION: Wherein Xaa is any naturally occurring amino acid
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2507 VSMFFYNDLVNGTTLQTRLGSKLLITASQDPLQPVQSRFVDGRAILQWDIFASNGIIHVI 2566
                                                      2454 -----EVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 2506
                        181 SLINFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPONSGLGENETLSGRDIEHHLAN
                                                                                                                       241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTBTRCVDGRDTLEWDICASNGITHVI
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ORGANISM: Rattus norvegicus
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US-09-842-930A-2
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US-09-842-930A-2
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
FILE REBERBERGE: 21402-22CIP
CURRENT APPLICATION NUMBER: 105/10/107,782

CURRENT FILING DATE: 2002-03-27
PRIOR PALICATION NUMBER: 10/028,248
PRIOR FILING DATE: 2001-12-19
PRIOR FILING DATE: 2001-12-19
PRIOR PLICATION NUMBER: 60/256,619
PRIOR FILING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-29
PRIOR PLING DATE: 2001-01-39
PRIOR PLING DATE: 2001-01-39
PRIOR PLING DATE: 2001-03-28
PRIOR PLING DATE: 2001-03-26
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; LOCATTON: (428)...(428)
... OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-10-107-782-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (55)...(55)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
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83.9%; Pred. No. 3.1e-159;
tive 5; Mismatches 16; Indels 36; Gaps
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                                                                                                                                                                                                                                     Taupier, Raymond, jr.
                                                                                                           Shimkets, Richard,
Si, Jingsheng,
Smithson, Glennda,
Spytek, Kimberly,
Stone, David,
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Vernet, Corine,
                      Patturajan, Meera,
Rothenberg, Mark,
Willet, Isabelle,
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                                                                Sciore, Paul,
Shenoy, Suresh,
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LOCATION: (55)...(55)
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LENGTH: 2675
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APPLICANT: WEIGEL, PAUL H
APPLICANT: WEIGEL, JANET A
TITLE OF INVENTION: METHODS OF USING THE HYALURONAN RECEPTOR FOR ENDOCYTOSIS
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weigel, Paul
TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
FILE REFERENCE: 5820.603
CURRENT APPLICATION NUMBER: US/09/842,930A
CURRENT FILING DATE: 2001-04-22
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR APPLICATION NUMBER: 60/245,320
PRIOR APPLICATION NUMBER: 60/199,538
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
SOFTWARE: Patentin version 3.1
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                                           2567 SRPLKAPPAPVTLTHTGLGAGIFFCIILVTGAVALAAYSYFRINRRTIGYQHF 2619
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301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353
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                                                                                                                                                                                                                                            Sequence 2, Application US/09842930A Publication No. US20020197681A1 GENERAL INFORMATION:
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121 QNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFSYSGNILQVIMSFP 180

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2423 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMK-----

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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                    121 QNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180
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79.3%; Pred. No. 2.5e-155;
.ive 29; Mismatches 43; Indels
         CURRENT APPLICATION NUMBER: US/10/133,172
CURRENT FILING DATE: 2002-04-25
FRIOR APPLICATION NUMBER: 60/286,468
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1431
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Kekuda, Ramesh
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Vernet, Corine
Casman, Stacie
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Shenoy, Suresh
Spytek, Kimberly
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Zerhusen, Bryan
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Millet, Isabelle
Rothenberg, Mark
                                                                                                                                                                  TYPE: PRT ORGANISM: Rattus norvegicus
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Edinger, Shlomit
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Boldog, Ferenc
                                                                                                                                                                                                                                           Best Local Similarity 79.3 Matches 280; Conservative
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Colman, Steven
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FILE REFERENCE: 5864.014
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TITLE OF INVENTION: No. US20030235882A1el Nucleic Acids and Polypeptides and Methods c
TITLE OF INVENTION: Thereof
FILE REPERENCE: 21402-222
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81.0%; Pred. No. 9.5e-152;
tive 4; Mismatches 27; Indels 36;
                                                                       THE KEREKENE 1410.7222

CURRENT FILING DATE: 010/10/028,248A

CURRENT FILING DATE: 2001-12-19

PRIOR PEDFLICATION NUMBER: 60/25619

PRIOR PELING DATE: 2000-12-19

PRIOR PILING DATE: 2001-01-9

PRIOR PILING DATE: 2001-01-9

PRIOR PILING DATE: 2001-01-9

PRIOR PILING DATE: 2001-01-9

PRIOR FILING DATE: 2001-02-28

PRIOR PILING DATE: 2001-04-20

PRIOR FILING DATE: 2001-04-20

PRIOR PILING DATE: 2001-04-20

PRIOR APPLICATION NUMBER: 60/2089

PRIOR APPLICATION NUMBER: 60/308039

PRIOR PILING DATE: 2001-07-26

PRIOR APPLICATION NUMBER: 60/311266

PRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 211
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APPLICANT: Casman, Stacie
APPLICANT: Colman, Steve,
APPLICANT: Edinger, Shlomit,
APPLICANT: Gangolli, Esha,
APPLICANT: Kekuda, Ramesh,
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Malyankar, Uriel,
Miller, Charles,
Millet, Isabelle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patturajan, Meera
Rothenberg, Mark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 286; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-028-248A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, Li
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US-10-107-782-39
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APPLICANT: Shenoy, Suresh,
APPLICANT: Shinkers, Richard,
APPLICANT: Shinkers, Richard,
APPLICANT: Shinkers, Richard,
APPLICANT: Shinkers, Richard,
APPLICANT: Shinkers, Richaerly,
APPLICANT: Spyrek, Kinberly,
APPLICANT: Spyrek, Kinberly,
APPLICANT: Stone, David,
APPLICANT: Carpier, Raymond, jr.,
APPLICANT: Carpier, Raymond, jr.,
APPLICANT: Carbien, Brian
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THERDOF
FILE REPERENCE: 21402-222CTP
TITLE OF INVENTION: NOVER: 2020-02-7
CURRENT APPLICANTION NUMBER: 00/28,48
PRIOR APPLICANTION NUMBER: 00/28,619
PRIOR FILING DATE: 2001-02-29
PRIOR FILING DATE: 2001-02-29
PRIOR PRILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/285,189
PRIOR PRILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/286,189
PRIOR APPLICATION NUMBER: 60/29,344
PRIOR APPLICATION NUMBER: 60/29,344
PRIOR APPLICATION NUMBER: 60/29,344
PRIOR APPLICATION NUMBER: 60/29,344
PRIOR APPLICATION NUMBER: 60/29,344
PRIOR APPLICATION NUMBER: 60/29,344
PRIOR PRILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PRIOR PRIOR VARIETION NUMBER: 60/29,344
PRIOR APPLICATION NUMBER: 60/29,344
PRIOR PRILING DATE: 2001-08-09
PRIOR PRIOR PRIOR VARIETION NUMBER: 60/29,344
PRIOR PRIOR PRIOR VARIETION NUMBER: 60/29,344
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PRIOR PRIOR PRIOR VARIETION NUMBER: 60/29,344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             817 QNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKG-------SAGLFQQLSSRP 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          861 CIS-------RTPDDLSIRGTLFVPQNSGLGENETLSGRDIEHHLAN 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGITHVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 VSMFFYNDLVNGTTLQTRLGSKLLITASQDPLQPTETRFVDGRAILQWDIFASNGIIHVI 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.4%; Score 1480; DB 15; Length 1069;
81.0%; Pred. No. 9.5e-152;
tive 4; Mismatches 27; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            961 SRPLKAPPAPVTLTHTGLGAGIFFAILLVTGAVALAAYSYFRINRRTIGFQHF 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: March 30, 2004, 15:48:18 Job time : 46 Becs
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Matches 286; Conservative
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CRGANISM: Homo sapiens
US-10-107-782-39
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No and

5.1.6
version
GenCore

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OM protein - protein search, using sw model

March 30, 2004, 15:38:31 ; Search time 21 Seconds
 (without alignments)
 1616.934 Million cell updates/sec Run on:

US-09-466-778B-11 1865 1 MTGPGKHKCECKSHYVGDGL.....ALAAYSYFRINRKTIGFXHF 353 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	н	hypothetical prote	•+	TSG-6 homolog PS4	hyaluronate-bindin	aggrecan precursor	proteoglycan core	aggrecan - bovine	proteoglycan link	proteoglycan link	brain link protein	proteoglycan link	aggrecan precursor	proteoglycan link	aggrecan precursor	proteoglycan link	aggrecan - pig (fr		brevican precursor	brevican precursor	neurocan precursor	brevican precursor	versican - pig-tai	chondroitin sulfat	versican precursor	versican precursor	brevican precursor	versican precursor	brevican precursor	
	А	T42681	JC6506	A47290	A41735	I50421	A28452	T42630	LKRT2	842938	JC7505	LKCH	A55182	LKHU	A39086	504243	529139	S52781	A53908	849126	S28764	A54423	843922	A47171	T14274	T42389	S57653	A60979		
	DB	2	N	~	7		7	7	, 1	Н	N	Н	٦	٦	Н	-4	N	~	N	~1	N	~	7	α,	7	7	N	Н	7	
	Query Match Length	1069	275	276	277	2109	2124	2327	408	354	340	355	2132	354	2415	354	370	1268	371	883	1257	912	862	3562	1643	3381	883	2409	378	
d	Query	79.4	14.2	4	4	4.6	9.2				8.9	6.8		8.8		8.7	9.8	8.5	8.4	8.4	8.4		8.3	8.3	8.1	8.1	8.1		7.9	
	Sco	1480	264	264	262	175	171	170	169.5	166.5	166	165.5	165	163.5	162	161.5	160	158.5	157.5	157.5	157.5	155.5		154.5		151.5	150.5	150.5	147	
	Result No.	1	7	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

proteoglycan core	chondroitin sulfat	T-cell surface gly	hypothetical prote	CD44 homolog membr	CD44R5 - human	lymphocyte surface	hypothetical prote	CD44 membrane glyc	slit protein 2 pre	slit protein 1 pre	fibrillin-2 precur	C-Delta-1 - chicke	hypothetical prote	protein F40E10.4 [intrinsic factor-B
A39808	A55885	A35616	T22674	A37009	177371	S24240	T34513	A34424	B36665	A36665	A57278	150719	T22025	D89711	T09456
7	7	~	7	7	7	~	7	~	0	01	ď	7	~	~	7
1340	113	362	1584	363	395	359	3507	365	1469	1480	2907	728	601	601	3623
7.5	6.5	5.9	5.8	5.8	5.7	2.6	5.6	5.5	5.4	5.4	5.4	5.3	5.3	5.3	5.3
139.5 7.5													99 5.3		98.5 5.3

ALIGNMENTS

RESULT 1 T42681 T42681 T42681 T42681 C:Deteical protein DKFZp434E0321.1 - human (fragments) C:Date: 11-Jan-2000_#sequence_revision 11-Jan-2000 #text_change 11-Jan-2000 C:Date: 11-Jan-2000_#sequence_revision 11-Jan-2000 #text_change 11-Jan-2000 C:Date: 11-Jan-2000_#sequence_revision 11-Jan-2000 #text_change 11-Jan-2000 C:Date: 11-Jan-2000_#sequence_revision 11-Jan-2000 C:Ancession: 126881 A:Restrict to the Protein Sequence Database, November 1999 A:Recession: T42681 A:Recession: T42681 A:Recession: T42681 A:Restrict to the Protein Sequence Database, November 1999 A:Recession: T42681 A:Recession: T42681 A:Restrict to the Protein Sequence Contains a +1 frameshift near codon 870 C:Genetics: A:Rote: DKFZp434E0321.1	Query Match 79.4%; Score 1480; DB 2; Length 1069; Best Local Similarity 81.0%; Pred. No. 1.4e-117; Matches 286; Conservative 4; Mismatches 27; Indels 36; Gaps 2;	1 MTGPGKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHL 60	61 RSPLGQYKLTFDKAREACANEAATWATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFAS 120	21 QNGGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVGYVGDGFSYSGNLLQVLMSFP 180	91 SLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPONSGLGENETLSGRDIEHHLAN 240 	11 VSMFFYNDLVNGTTLQTRLGSKLLITDRQDPLHPTETRCVDGRDTLEWDICASNGTTHVI 300
RESULT 1 T42681 Cypethetical protein Cypethetical protein Cypethetical brotein Cypethetical Language Cypate: 11-Jan-2000 Cypate: 11-Jan-2000 Cypate: 11-Jan-2000 Cypate: 11-Jan-2000 Cypate: 11-Jan-2000 Cypate: 11-Jan-2000 Cypethetical type: Protein Cypate Cypate: 17-September: Aykoleulus; 1-870; 81 Aykote: the CDN see Cygenetics: Cygenetics: Aykote: DKFZp434503	Query Match Best Local Matches 28	, 69	61	121	181	241
NESULT 142681 hypoto C;Spec C;Date C;Date C;Date R;Blum R;Blum R;Blum R;Blum R;Blum R;Refe A;Role A;Role A;Role A;Role A;Role A;Role A;Role A;Role A;Role A;Role A;Role A;Role	δă¤	δ. dg	Oy Op	yy a	Sy di	Qy

RESULT 2 JC6506

tumor necrosis factor stimulated gene-6 protein - mouse C,Species: Mus musculus (house mouse)

301 SRXLKAPPAPVTLXHTGLGXGIFXXIILVTGAVALAAYSYFRINRKTIGFXHF 353

q δ g

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A; Molecule type: mRNA
A; Residues: 1-277 <LEES
A; Cross-references: GB:M31165; NID:g339994; PIDN:AAB00792.1; PID:g1332377
A; Experimental source: FS-4 fibroblast
A; Experimental source extracted from NCBI backbone (NCBIN:76828, NCBIP:76833)
R; Wishiewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
B; Chemistry 33, 7423-7429, 1994
A; Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comple A; Reference number: A53642; MUID:94271799; PMID:7516184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-361, DL', 364-600, R', 602-999, R', 1001-1028, P', 1030-1250, D', 1252-1549, T',
A;Cross-references: EMBL: M88101
R;Sai, S.; Tanaka, T.; Kosher, R.A.; Tanzer, M.L.
Proc. Natl. Acad. Sci. U.S.A. 83, 5081-5085, 1986
                    J. Cell Biol. 116, 545-557, 1992
A;Title: A novel secretory tumor necrosis factor-inducible protein (TSG-6) is a member of A;Reference number: A41735; MUID:92112993; PMID:1730767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NyAlternate names: cartilage chondroitin sulfate proteoglycan core protein C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000
R; Li, H.; Schwartz, N.B.; Vertel, B.M.
J; Biol. Chem. 268, 23504-23511, 1993
A; Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-361,'DL',364-600,'R',602-999,'R',1001-1028,'P',1030-1250,'D',1252-1602,'A'
A;Cross-references: GB:M88101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 ERAAGVYHREARSGKYKLTYAEAKAVCEFEGGHLATYKQLEAARKIGFHVCAAGWMAKGR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C)Superfamily: Cir/Cis repeat homology, link protein repeat homology C,Superfamily: Cir/Cis repeat homology, consequence (S,Eqwords: alycoprotein (S,E,L-19,Domain: signal sequence #status predicted <SIG> F):1-19,Domain: signal sequence binding protein TSG-6 #status predicted <MAT> F):20-277/Product: hyaluromate-binding protein TSG-6 #status predicted <MAT> F):31-284/Domain: link protein repeat homology <CIR2> F):185-244/Domain: CIr/Cis repeat homology <CIR2> F):185-244/Domain: CIr/Cis repeat homology <CIR2> F):18,558/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A;Residues: 1-2109 <LIX>
A;Cross-references: GB:L21913; NID:g416133; PIDN:AAB19128.1; PID:g416134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Biochem. J. 288, 903-910, 1992
A;Title: Molecular cloning of chicken aggrecan. Structural analyses.
A;Reference number: S27356; MUID:93111968; PMID:1339285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 262; DB 2; Length 277; 43.3%; Pred. No. 1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 VAYPTAFASQNCGSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 VGYPIVKPGPNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Reference number: A48884; MUID:94043149; PMID:8226878
A.Accession: IS0421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A;Reference number: S39796; MUID:94107258; PMID:8280087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches
T.H.; Wisniewski, H.G.; Vilcek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.3%;
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Best Local Similarity
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                                                                                                                                                          A; Accession: A41735
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A;Note: this report replaces the sequence from reference A47290 and shares no similarity Ferg, P.; Liau, G.
T. Enol. Chem. 268, 9387-9392, 1993
A;Title: Identification of a novel serum and growth factor-inducible gene in vascular sm A;Reference number: A47290; MUID:93252803; PMID:8098034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: vascular smooth muscle cells
A;Note: sequence extracted from NCBI backbone (NCBIN:131589, NCBIP:131590)
A;Note: the sequence exported here was found to be artifactual, a hybrid molecule of two
C;Superfamily: Clr/Cls repeat homology; link protein repeat homology
F;53-128/Domain: link protein repeat homology <LNC:
F;135-244/Domain: Clr/Cls repeat homology <CIR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NiAlternate names: probable cell growth and differentiation protein, 12K; serum-inducible (Species: Orycotolagus cuniculus (domestic rabbit)
C; Species: Orycotolagus cuniculus (domestic rabbit)
C; Species: 03-Mar-1994 #sequence_revision 07-Jul-1995 #text_change 08-Oct-1999
C; Accession: A48055; A47290
J; Reng, P.; Liau, G.
J; Liau, G.
A; Reng, P.; Liau, G.
A; Reference number: 268, 21453, 1993
A; Reference number: A48055; MUID:94012707; PMID:8407990
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A;Molecule type: mRNA
A;Residues: 'MEGSNRKSQLTTEDVALDGWTCRKNSFVLTVVRTNGLYAALVSLGNRRRPGVTVQRTEGNFSSRHESCAREPALQ
                                                                         T.T
                                                                                                                                                      A,Title: Coding sequence, exon-intron structure and chromosomal localization of murine A,Reference number: JC6506, MUID:98087423; PMID:9427551
                                                        R;Fueloep, C.; Kamath, R.V.; Li, Y.; Otto, J.M.; Salustri, A.; Olsen, B.R.; Glant, Gene 202, 95-102, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 DTTVGVFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 EQAAGVYHREARAGRYKLTYAEAKAVCEFEGGRLATYKQLEAARKIGFHVCAAGWMAKGR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyaluronate-binding protein TSG-6 precursor - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
C;Accession: A41735; D53642
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:U83903; NID:g2062474; PIDN:AAC53527.1; PID:g2062475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 275;
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43.3%; Pred. No. 6.7e-15;
tive 16; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 VGYPIVKPGPNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAKEC 135
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43.3%; Pred. No. 6.7e-15;
tive 16; Mismatches 43;
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les 45; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                               A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-275 <FUE>
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                                            C; Accession: JC6506
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A,Title: Cloning and sequence analysis of a partial cDNA for chicken cartilage proteogly A,Reference number: A25442; MUID:86259736; PMID:3460082 A;Accession: A25442; MUID:86259736; PMID:3460082 A;Accession: A25442; MUID:86259736; PMID:3460082 A;Accession: A25442; MUID:86259736; PMID:3460082	Qy 226NETLSGRDIEHHLANVS 242 :
95, 'G' GB:M1 Ge: st	LT 6 52 bodlycan core
A. Biol. Chem. 263, 15831-15835, 1981-15835. And Continued of the gene for chicken cartilage proteoglycan core protein. A;Title: Partial structure of the gene for chicken cartilage proteoglycan core protein. A;Reference number: A32002; MUID:89008500; PMID:3170613	Core process processor, cartiage fractiones: aggreen strue norvegices (Norway rat) nn-1989 #sequence_revision 30-Jun-1989 #text_chan A92623; A23835; A28453; A28095; A28452
A.Molecule type: DNA A.Residues: 1893-1987,'S',1989-2022 <tan> A.Note: the authors translated the codon TCC for residue 1787 as Phe B.Krieger P.C.</tan>	R,Doege, K.; Sasaki, M.; Horigan, E.; Hassell, J.R.; Yamada, Y. J. Biol. Chem. 262, 17757-17767, 1987 A;Title: Complete primary structure of the rat cartilage proteoglycan core protein deduce b.Deference number. 197623. WITTD.BR087070. DMTD.369370
J. Biol. Chem. 265, 12088-12097, 1990 A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein: II. Nucleotide s A:Reference number: I50216; MUID:90307744; PMID:1694853	
A.Accesion: 150216 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA	R.Doege, K.; Sasaki, M.; Horigan, E.; Habsell, J.R.; Yamada, Y. J. Biol. Chem. 263, 10040a, 1988 A.Reference number: A30069
A;Residues: 'PA',1044-1559 <kru> A;Cross-references: GB:M38187; NID:g211685; PIDN:AAA48731.1; PID:g555441 R;Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.</kru>	98 Saki, M.; Yamada, Y.
J. Biol. Chem. 265, 12075-12087, 1990 A;Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation an A;Reference number: A37072; MUID:90307743; PMID:2365711	A.Title: Partial cDNA sequence encoding a globular domain at the C terminus of the rat ci A.Reference number: A23835; MUID:86250698; PMID:2424893 A.Accession: A23835
A;Accession: A370;7 A;Molecule type: protein A;Residues: 998-1015,′X′,1017-1019,′X′,1021-1023 <kr2> A;Note: amino end of 86K core peptide CS-A</kr2>	A;NOLECLIE LYDE: mrwa. A;Residues: 1856-21244 <do2> A;Cross-references: GB:M13518; NID:9206104; PIDN:AAA41836.1; PID:9206105 R;Neame, P.J.; Christner, J.E.; Baker, J.R.</do2>
A; Molecule type: protein A; Molecule type: protein A; Mesidues: 1247-1250, 'D', 1252-1272,'X', 1274-1275 < KR3>	J. Biol. Chem. 262, 17768-17778, 1987 A,Title: Cartilage proteoglycan aggregates. The link protein and proteoglycan amino-term: A,Reference number: A28453; MUID:88087071; PMID:3693371
Association of the following states of the following states of the following states of the following states of the following specific states of the following states of the fo	A; Molecule type: protein A; Molecule type: protein A; Residues: 20-37, W', 39-60, E', 62-64, X', 66-69; 70-83; 84, 89-148, 'L', 150-238, 'S', 240, 'A', '. C; Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EGI
F;21-2109/Product: aggrecan #status predicted <mat> F;41-31/Domain: immunoglobulin bomology <lmm> F;46-243/Domain: link protein repeat homology <lnk1> F:264-346/Domain: link protein repeat homology <lnk2></lnk2></lnk1></lmm></mat>	C.Keywords: glycoprotein F;1-19/Domain: signal sequence #status predicted <sig> F;20-2124/Product: proteoglycan core protein #status predicted <mat> F:44-135/Domain: immunoclobulin homology <imm></imm></mat></sig>
F;S37-614/Domain: link protein repeat homology <lnk3> F;635-716/Domain: link protein repeat homology <lnk4> F;1859-1890/Domain: EGF homology <egf> F:1807-2011/Domain: C-two lectin homology <</egf></lnk4></lnk3>	F;170-247/Domain: link protein repeat homology <lnk1> F;268-349/Domain: link protein repeat homology <lnk2> F;368-381/Domain: link protein repeat homology <lnk3> F;304-581/Domain: link protein repeat homology <lnk3> F:307-503/homain: link protein repeat homology <lnk3></lnk3></lnk3></lnk3></lnk2></lnk1>
F;2024-2080/Domain: C-type rectin nomorogy vern> F;2024-2080/Domain: complement factor H repeat homology <fhd> Ouery Match 9.4%; Score 175; DB 1; Length 2109;</fhd>	F;002-003/DOMMAIN: LIN PICCEIN TEPEAC HOMOJOGY CLARY F;1914-2034/Dommain: Crype lectin homology cLGH> F;2041-2037/Dommain: Complement factor H repeat homology <fhd> F:126,239,333,387,611,667,1842/Binding site: carbohydrate (Asn) (covalent) #status predic</fhd>
Best Local Similarity 23.4%; Pred. No. 3.2e-06; Matches 75; Conservative 31; Mismatches 116; Ind	4;
QY 10 BCKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVG 56	57
57	Db 488 VFHYRPGSTRYSLTFEBAQQACIRTGAAIASPEQLQAAYEAGYBQCDAGWLQDQTVRYFI 547
Db 251 VFYATSPEKFTFQEAFDKCHSLGARLATTGELYLAWKDGMDMCSAGWLADRSVRYFI 307 Qy 117 AFASQNCGSGVVGIVDYGPRPNKSEMMDVFCYRMKDVNCTXKVG-YV 162	Qy 117 AFASQNCGSGVVGIVDYGPRPNKSEMWDVPCYRMKDVNCTXKVGYVGDGFSYSGNLL 173
Db 308 SRARPNCGGNLVGVRTVXINPANQTGYPHPSSRYDAICYSGDDFEALVPGLFTDEVGTEL 367 OV 163 GDGFSVSAGNIOVIMSEDSTFUEL 186	Qy 174 QVLMSPPSLTNFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGL 223 Dh
368 GSAFTIQTVTQTEVELPLPRNVTEBBARGSIATLEPWEITATATELYBAFTVLPDLFA 42	С 4.111.12
Qy 187 TEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGLGE 225	a

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brain link protein-1 - human (man) (cjspecies: Homo sapiens (man) (cjspecies: Homo sapiens (man) (cjspecies: Homo-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000 (cjscession: JC7505 R.H.; Nu.D.; Yoshioka, H.; Murakami, T.; Arata, J.; Ninomiya, T.; Hirakawa, S.; Oohashi, T.; Su, W.D.; Yoshioka, H.; Murakami, T.; Arata, J.; Ninomiya, T.; Aritle: The brain link protein-1 (BRAL1): cDNA cloning, genomic structure, and characte: A;Reference number: JC7505
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A; Cross-references: BMBL:X78077; NID:9459438; PIDN:CAA54987.1; PID:9459439
C; Superfamily: proteoglycan link protein; immunoglobulin homology; link protein repeat ht C; Keywords: cartilage; duplication; extracellular matrix; glycoprotein F;1-15/Domain: signal sequence #status predicted <SIG>F;1-15/Domain: signal sequence #status predicted <SIG>F;16-354/Product: proteoglycan link protein #status predicted <MAT>
F;54-141/Domain: immunoglobulin homology <IMM>
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C;Keywords: brain; tandem repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 GQYKLIFDKARBACANBAATWATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 GRYNLNFHEAQQACLDQDAVIASFDQLYDAWRGGLDWCNAGWLSDGSVQYPITKPREPCG 227
                                                                                                                                                                           GOYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCG 124
                                                                 --EDDIAVVALELQGV---VFPYFPRL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GYHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: cartilage link protein
C;Species: Equus caballus (domestic horse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Jun-1999
GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;176-253/Domain: link protein repeat homology <LNK1>
F;274-350/Domain: link protein repeat homology <LNK2>
F;21,56/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;51,57/Pisulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

8.9%; Score 166.5; DB 1
Best Local Similarity 30.1%; Pred. No. 1.8e-06;
Matches 44; Conservative 22; Mismatches 51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Dudhia, J.; Platt, D.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 -- SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 GONTVPGVRNÝGFWDKEKSRYDVFCF 253
                                                                                                                                                                                                                                                                125 --SGVVGIVDYGPRPNKSEMMDVFCY 148
                                                                                                                                                                                                                                                                                                                              282 GONTVPGVRNYGFWDKDKSRYDVFCF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteoglycan link protein precursor - horse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: DDBJ:AB049054
                                                                 189 GRYKCE-----VIEGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 GRYKCE----VIEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-340 <HIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-354 < DUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JC7505
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JC7505
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A;Accession: A28680
A;Rocioule type: mRNA
A;Residues: 180-408 - ADE>
R;Neame, P.J.; Christner, J.E.; Baker, J.R.
A; Biol. Chem. 261, 351-3555, 1986
A;Title: The primary structure of link protein from rat chondrosarcoma proteoglycan aggr
A;Reference number: A02869; MUID:86140139; PMID:2419334
          C,Accession: T42630
MyHering, T.M.; Kollar, J.; Huynh, T.D.
submitted to the EMBL Data Library, September 1996
A,Description: Complete coding sequence of bovine aggrecan: comparative structural analy
                                                                                                                                                                                                                                                                                                                                     A;Experimental source: articular chondrocytes
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: cartilage; chondroitin sulfate proteoglycan; extracellular matrix; glycoprof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protegglycan link protein 2 precursor - rat
NiAlternate names: cartilage link protein
NiAlternate names: cartilage link protein
Cipecies Rattus norvegicus (Norway rat)
Cipecies: 13-Aug-1986 #sequence revision 24-Oct-1997 #text_change 13-Nov-1998
CiAccession: A28654; A24880; Ā02869
CiAccession: A28654; A24880; Ā02869
Circassion: C.; Doege, K.; Sasaki, M.; Yamada, Y.
J. Balol. Chem. 263, 6063-6067, 1988
A;Title: Alternative splicing generates two different mRNA sepcies for rat link protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A28654
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-408 «RHO>
R;Doege, K.; Hassell, J.R.; Caterson, B.; Yamada, Y.
R;Doege, K.; Hassell, J.R.; Caterson, B.; Yamada, Y.
A;Title: Link protein cDNA sequence reveals a tandemly repeated protein structure.
A;Reference number: A24880; MUID:86233314; PMID:3459153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;230-307/Domain: link protein repeat homology <LNK1>
F;228-404/Domain: link protein repeat homology <LNK2>
F;110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;115-193,235-306,259-280,333-403,358-379/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 VPHYRPGSSRYSLÍFEEAKQACLRIGALIASPEQLQAAYEAGYEQCDAGWLQDQTVRYPI 547
                                                                                                                                                                       A,Accession: T42630
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-2327 <HER>
A,Residues: 1-2327 <HER>
A,Cross-references: EMBL:U76615; NID:g1730259; PID:g1730260; PIDN:AAB38524.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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30.8%; Pred. No. 1.2e-06;
rative 20; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AFASONC---GSGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 VSPRTPCVGDKDSSPGVRTYGVRP-PSETYDVYCY 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.1%; Score 170; DB 2;
38.9%; Pred. No. 9.7e-06;
cive 12; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 38.9
                                                                                                                                            A; Reference number: Z22182
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Best Local Similarity
Matches 45; Conserv:
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Best Local S:
Matches 37,
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Gaps

29.

Indels

Conservative

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63

us-09-466-778b-11.rpr

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aggrecan precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 21-Jan-2000
C;Accession: A55182; 855329; $50207; 851355; 178532; 158123
R;Walcz, E; Deak, F; Erhardt, P.; Coulter, S.N.; Fueloep, C.; Horvath, P.; Doege, K.J.
Genomics 22, 364-317, 1994
A;Fitle: Complete coding sequence, deduced primary structure, chromosomal localization, A;Reference number: A55182; MUID:95104847; PMID:7806222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Residues: 1-2132 <WAL>
A,Cross-references: GB:L07049; NID:g678541; PIDN:AAC37670.1; PID:g191772
A;Cross-references: GB:L07049; NID:g678541; PIDN:AAC37670.1; PID:g191772
B;Matcanabe, H.; Gao, L.; Sugiyama, S.; Doege, K.; Kimata, K.; Yamada, Y.
Biochem. J. 308, 433-440, 1995
A;Title: Mouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structural, Rouse aggrecan, a large cartilage proteoglycan: protein sequence, gene structural, A;Reference number: S55329; MUID:95289972; PMID:7772024
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Ajtitle: Mouse cartilage matrix deficiency (cmd) caused by a 7 bp deletion in the aggrec A;Reference number: 158123; MUID:95004579; PMID:7920633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 211-240,'MCTASLRRWRVRSFWRHPQRNSPSRRQPTS','AGGWGHAWPPQASSTWPGRAVWTCAALAGW','R
A;Cross-references: GB:S73720; NID:9765211; PIDN:AAB32159.1; PID:9765212
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C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; BG
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A;Cross-references: GB:U22001; NID:9886014
R;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Titles: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by A;Reference number: S50206; MUID:95035091; PMID:7524681
                                                                                                                                                                                                                 ---EDDTAVVALNLE----GVVFPYSPR 167
                                                                                                                                                           64 LGQYKLTFDKAREACANEAATMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSP-
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                                                                                                                                                                                                                                                                                                                      124 G--SGVVGIVDYGPRPNKSEMWDVFCY 148
                                                                                                                                                                                                                                                                                                                                                                                                     228 GGKNTVPGVRNÝGFWDKERSRYDVFCF 254
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A;Residues: 350-481,'R',483-506 <GLU1>
A;Cross-references: EMBL:X80279; NID:g673432
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A,Residues: 350-383,'CPVMSQRERPWAA' <GLU2>
A,Cross-references: EMBL:X80279
                                                                           136 GRYKCE----VIEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 211-326 < WAT2>
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A; Status: preliminary
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C:Species: Gallus gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Date: 28 Dec-1987 #sequence revision 28-Dec-1987 #text_change 22-Jun-1999
C:Accession: A28305; A24881; A33097; B39097
R:Kiss, I.; Deak, F.; Mestric, S.; Delius, H.; Soos, J.; Dekany, K.; Argraves, W.S.; Spa Proc. Natl. Acad. Sci. US.A. 84, 6399-6403, 1987
A;Title: Structure of the chicken link protein gene: exons correlate with the protein dc A;Reference number: A28305; MUID:87317659; PMID:3476955
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A; Residues: 1-355 < DEB.>
A; Residues: 1-355 < DEB.>
A; Residues: 1-355 < DEB.>
A; Cross=r-references: GB:M13212; NID:g212259; PIDN:AAA48940.1; PID:g212260
A; Experimental source: embryonic sternal cartilage
B; Wu, L.N.Y.; Genge, B.R.; Wuthier, R.E.
A; Biol. Chem. 266, 1187-1194, 1991
A; Title: Association between proteoglycans and matrix vesicles in the extracellular matr
A; Reference number: A39097; MUID:91093230; PMID:1985942
A; Accession: A39097
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A,Residues: 40-55, X',57-59 <WU2>
A,Note: 38 protein, a minor component of matrix vesicles
C,Comment: Link proteins stabilize the aggregates of proteoglycan monomers with hyaluron
tructures that induce mineralization).
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R;Deak, F.; Kiss, I.; Sparks, K.U.; Argraves, W.S.; Hampikian, G.; Goetinck, P.F.
Proc. Natl. Acad. Sci. US.A. 83, 3766-3770, 1986
A;Title: Complete amino acid sequence of chicken cartilage link protein deduced from CDN
A;Reference number: A24881; MUID:86233315; PMID:3459154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A;Residues: 40-55,'X',57-60,'X',62-75,'X',77-78,'X' <WUA>
A;Note: 38K protein, a major component of matrix vesicles; Asn-56 appears to be glycosy.
A;Accession: B39097
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(S. Superfeamily: proteoglycan link protein; immunoglobulin homology; link protein repeat
(S. Superfeamily: proteoglycan link protein; extracellular matrix; glycoprotein
(S. Superfeamily: protein; duplication; extracellular matrix; glycoprotein
(S. Startilage; duplication; extracellular matrix; glycoprotein
(S. 11-15/Domain: signal sequence #status predicted <NAT>
(S. 142/Domain: link protein #status predicted <NAT>
(S. 142/Domain: link protein repeat homology <NAT>
(S. 142/Domain: link protein repeat homology <NAT>
(S. 142/Diplication; link protein repeat homology <NAT>
(S. 142/Diplication; link protein repeat homology <NAT>
(S. 142/Diplication; link protein (S. 142/Diplication) (Covalent) #status experimental
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                                                                                                                                                                                                                                                           84 IMATYNQLSYXQKAKYHLCSAGWLETGRVAYPTAFASQNCGS-GVVGIVDYGPRPNKSEM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 RIATYSOLYQAWTEGLDWCNAGWLLEGSVRYPVLTARAPCGGRGRPGIRSYGPRDRMRDR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :61-140,182-253,206-227,280-350,305-326/Digulfide bonds: #status predicted
                                                                                                                                                                                                         ---VFHLRSPLGQYKLTFDKAREACANEAA
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                                                                                                                             Gaps
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                                                  Length 340;
                                                                                                                                 51; Indels
                                              8.9%; Score 166; DB 2;
31.7%; Pred. No. 1.9e-06;
trive 21; Mismatches 51;
                                                                                                                                                                                                             33 LQDNGQCHADAKCVDLH-FQDTTVG-
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                                                                                                                                 40; Conservative
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                                                  Query Match
Best Local Similarity
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 WDVFCY 148
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A;Residue=: 1.216.2.201-2329,'A',2392-2415 <DOE>
A;Cross-references: GB:M55122; NID:g178258; PIDN:AAA62824.1; PID:g178259
B;Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.
Biochim. Biophys. Acta 1219, 613-622, 1994
A;Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by l
A;Reference number: S50206; MuID:95035091; PMID:7524681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggrecan precursor, cartilage long splice form [validated] - human N.Alternate names: chondroitin sulfate proteoglycan 1; large aggregating proteoglycan; ph. N.Contains: aggrecan cartilage short splice form C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Pate: 10-Sep-1999 #sequence revision 01-Dec-2000 #text_change 08-Dec-2000 C;Accession: A39086; SS0206; A43919; S46659; S66389; S68646; S62786; A34226; B43919; C43: R;Doege, K.J.; Saaski, M.; Kimura, T.; Yamada, Y. J. Biol. Chem. 266, 894-902, 1991 A;Title: Complete coding sequence and deduced primary structure of the human cartilage 1: A; Afference number: A39086; MUID:91093289; PMID:1985970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: proteoglycan link protein; immunoglobulin homology; link protein repeat hc C;Keywords: cartilage; duplication; extracellular matrix; glycoprotein F;1-15/Domain: signal sequence #status predicted <SIG> F;1-534/Product: proteoglycan link protein #status experimental <MAT> F;54-141/Domain: immunoglobulin homology <IMA> F;176-253/Domain: link protein repeat homology <IMA> F;176-253/Domain: link protein repeat homology <IMA> F;176-253/Domain: link protein repeat homology <IMA> F;176-253/Domain: link protein repeat homology <IMAZ> F;275-253/Domain: link protein repeat homo
                                                                        A,Title: Cartilage proteoglycan aggregate is degraded more extensively by cathepsin L that A,Reference number: S09309; MUID:90197639; PMID:2317204
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A,Title: The structure of aggrecan fragments in human synovial fluid. Evidence for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNÅ
A;Residues: 350-497 <GLU>
A;Cross-references: EMBL:X80278; NID:G516295
A;Cross-references: EMBL:X80278; NID:G516295
A;Note: this translation is not annotated in GenBank entry HSAGGREC, release 113.0
B;Sandy, J.D.; Flannery, C.R.; Neame, P.J.; Lohmander, L.S.
U. Clin. Invest. 89, 1512-1516, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GKHKCECKSHYVGDGLNCEPEQLPIDRCLQDNGQCHADAKCVDLHFQDTTVGVFHLRSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;21,56/Binding site: carbohydrate (Asn) (covalent) #status predicted F;61-139/Disulfide bonds: #status predicted
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A;Molecule type: protein
A;Residues: 361-370,'X',372-373;393-399,'X',401-407,'X',409 <SAN>
                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 16-38,'X',40-55,57-60,62-65,'X',67,'X',69-80 <NG2>
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8.8%; Score 163.5; DB 1;
Best Local Similarity 30.1%; Pred. No. 3.2e-06;
Matches 44; Conservative 21; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GDB:125232; OMIM:115435
A,Map position: 5q13-5q14
Q.; Mort, J.S.; Roughley, P.J.
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                                                266, 569-573, 1990
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A;Title: Appendix. Isolation and sequence of CDNA clones for pig and human cartilage lin A;Reference number: S04243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riosborne-Lawrence, S.L.; Sinclair, A.K.; Hicks, R.C.; Lacey, S.W.; Eddy Jr., R.L.; Byer Genomics 8, 562-567, 1990
A; Title: Complete amino acid sequence of human cartilage link protein (CRTL1) deduced fr
A; Reference number: A36308; MUID:91139126; PMID:2286376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. Molecule type: mANA
A. Molecule type: mANA
A. Residues: 223-354 sDUD2>
A. Krosse-references: EMBL:Y00166
A. Note: the authors translated the codon CTG for residue 264 as Arg and TTG for residue
R. Nguyen, Q.; Murphy, G.; Roughley, P.J.; Mort, J.S.
B. Ochem. J. 259, 61-67, 1989
A. Title: Degradation of proteoglycan aggregate by a cartilage metalloproteinase. Evidenc
A. Reference number: S03868; MUID:89246328; PMID:2719651
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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
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M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AFASQNÇ---GSGVVGIVDYGPRPNKSEMWDVFCYRMKDVNCTXKVGYVGDGFSYSGNLL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NyAlternate names: cartilage link protein

Cispecies: Homo sapiens (man)

Cispecies: Homo sapiens (man)

Cispecies: 31-Dec-1991 #sequence revision 31-Dec-1891 #text change 08-Dec-2000

Cispecies: 31, Pardingham, T.E.

Ribudhia, J.; Hardingham, T.E.

Nucleic Acids Res. 18, 1292, 1990

A;Fitle: The primary structure of human cartilage link protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Residues: 1-354 <DUD>
A;Cross-references: EMBL:X17405; NID:g463246; PIDN:CAA35462.1; PID:g34378
A;Note: the authors translated the codon GAT for residue 93 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 VSPRTPCVGDKDSSPGVRTYRVRPS-SETYDVYCYVDK-----LEGEVF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 OVLMSFPSLINFLTEVLAYSNSSARGRAFLEHLTDLSIRGTLFVPQNSGL 223
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R,Dudhia, J.; Hardingham, T.E.
Nucleic Acids Res. 18, 2214, 1990
A,Title: The primary structure of human cartilage link protein.
A,Reference number: S14926; MUID:90245703; PMID:2336413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ee; Indels
                                                F;170-247/Domain: link protein repeat homology <LNK1>
F;268-349/Domain: link protein repeat homology <LNK2>
F;604-581/Domain: link protein repeat homology <LNK3>
F;602-683/Domain: link protein repeat homology <LNK4>
F;1922-2042/Domain: C-type lectin homology <LK4>
F;2049-2105/Domain: complement factor H repeat homology <FHD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteoglycan link protein precursor [validated] - human
                                                                                                                                                                                                                                                                                                                                                                            Match 8.8%; Score 165; DB 1; Local Similarity 28.8%; Pred. No. 2.3e-05; les 49; Conservative 23; Mismatches 66.
                   F;44-135/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-92,'A',94-354 <NUC>
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Best Local S:
Matches 49
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Search completed: March 30, 2004, 15:43:02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S04243; 147145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-354 < DUD>
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F;126,239,333,387,434,602,657,737,1898/Binding site: carbohydrate (Asn) (covalent) #stat
F;371,376/Binding site: keratan sulfate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1778-1927, A, 1929-1963, VV, 1965-2162,2201-2415 <DUD>
A; Residues: 1778-1927, A, 1929-1963, VV, 1965-2162,2201-2415 <DUD>
A; Cross-references: EMBL:XI7406, NID:930248; PIDN:CAA35463.1; PID:930249
A; Cross-references: EMBL:XI7406, NID:930248; PIDN:CAA35463.1; PID:930249
A; Raldwin, C.T.; Reginato, A.M.; Prockop, D.J.
Baol. Chem. 264, 1574-15750, 1989
A; Title: A new epidemmal growth factor-like domain in the human core protein for the lax
A; Reference number: A34226; MUID:89380154; PMID:2789216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Map position: 15q26-15q26
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Superfamily: aggrecan; C-type lectin homology; condition sulfate proteoglycan; extracell
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-2415/Product: aggrecan cartilage long splice form #status predicted <MATL>F;20-2415/Product: aggrecan cartilage short splice form #status predicted <MAT = 15,0-2162,2210-2415/Product: aggrecan cartilage short splice form #status predicted <MATR>F;20-2162,2210-2329, 'A',2332-2415/Product: aggrecan short splice form #status predicted F;44-135/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Modecule type: protein
A; Residues: 'V', 404-405,'XX' <FOS>
R; Budhia, J; Davidson, C.M.; Wells, T.M.; Vynios, D.H.; Hardingham, T.E.; Bayliss, M.T.
Bochem. 3131, 933-940, 1996
A;Title: Age-related changes in the content of the C-terminal region of aggrecan in huma A; Reference number: $62786; MUD:96190740; PMID:8611178
A;Cross-references: PIDN:AAB22079.1; PID:g248644; PIDN:AAB22077.1; PID:g248842; PIDN:AAB
A;Experimental source: synovial fluid
A;Note: sequences modified after extraction from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 764-765, A',767-846, VV, 848-862, XY, 864 <BAR>
A; Cross-references: EMBL:S74659; NID:9807127; PIDN:AAGG0643.1; PID:9807128
A; Cross-references: EMBL:S74659; NID:9807127; PIDN:AAGG0643.1; PID:9807128
A; Note: the authors translated the codon GAA for residue 803 as Ala and CYT for residue
R; Ilic, M.Z.; MoK, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.B.; Handley, C.J.
A; Tilic, M.S.; MoK, M.T.; Williamson, O.D.; Campbell, M.A.; Hughes, C.B.; Handley, C.J.
A; Title: Catabolism of aggrecan by explant cultures of human articular cartilage in the
A; Reference number: 866389; MUID:9604775; PMID:7574678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                         R.Barry, F.P.; Neame, P.J.; Sasse, J.; Pearson, D.
Matrix Biol. 14, 323-328, 1994
Agritle: Length variation in the Keratan sulfate domain of mammalian aggrecan.
A,Reference number: 146998; MUID:95128522; PMID:7827755
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Fi268-349/Domain: link protein repeat homology <LNK2>
Fi268-349/Domain: link protein repeat homology <LNK3>
Fi393-673/Domain: link protein repeat homology <LNK4>
Fi503-673/Domain: keratan sulfate attachment #status predicted <KSA>
Fi677-861/Domain: keratan sulfate attachment #status predicted <KSA>
Fi864-1510/Domain: chondroitin sulfate attachment #status predicted <CS1>
Fi1511-2162/Domain: chondroitin sulfate attachment #status predicted <CS2>
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Cross-references: GB:J05062; NID:9181167; PIDN:AAA35726.1; PID:9181168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 17-23;24,'X',26-27;393-401;402-403 <LLI>A;Residues: 17-23;24,'X', 26-27;393-401;402-403 <LLI>CR;Fosang, A.J.; Last, K.; Knaeuper, V.; Murphy, G.; Neame, P.J.
FEBS Lett. 380, 17-20, 1996
A;Title: Degradation of cartilage aggrecan by collagenase-3 (MMP-13).
A;Reference number: S68646; MUID:96181659; PMID:8603731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%; Score 162; DB 1; Length 2415; 6.5%; Pred. No. 4.9e-05;
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A)Cross-references: GDB:127479; OMIM:155760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2168-2198/Domain: EGF homology <EGF>
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Residues: 1936-1963,
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Best Local S
Matches 63
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10;

Gaps

68;

82; Indels

25; Mismatches

Local Similarity 26.5%; Conservative

63;

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A;Cross-references: EMBL:Y00165; NID:92009; PIDN:CAA68358.1; PID:92010
C;Superfamily: proteoglycan link protein; immunoglobulin homology; link protein repeat ha C;Keywords: cartilage; duplication; extracellular matrix; glycoprotein P;1-15/Domain: signal sequence Hatatus predicted <SIG-554/Product: proteoglycan link protein Hatatus predicted <NGT>
F;54-141/Domain: immunoglobulin homology <NMM>
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R;Perkins, S.J.; Nealis, A.S.; Dudhia, J.; Hardingham, T.E.
Nol. 26, 737-733, 1989
A;Title: Immunoglobulin fold and tandem repeat structures in proteoglycan N-terminal dom:
A;Reference number: I47145; MUID:89293837; PMID:2738916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R, Dudhia, J.; Hardingham, T.E.
J. Mol. Biol. 206, 749-753, 1989
A, Title: Appendix. Isolation and sequence of CDNA clones for pig and human cartilage lin.
A, Reference number: S04243
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                                                                160 DLVVQVTAVPGQPHLPGGVVFHYRPGPTRYSLTFEEAQQACPGTGAVIASPEQLQAAYEA 519
                                                                                                                                        98 KYHLCSAGWLETGRVAYPTAFASQNC---GSGVVGIVDYGPRPNKSEMWDVFCY---- 148
                                                                                                                                                                                      579 EVFFATRLEQFTFQEALEFCESHNATATTGQLYAAWSRGLDKCYAGWLADGSLRYPIVTP 638
                                                                                                                                                                                                                                                                                        149 -----RMKDV------NCTXKVGYVGDGFS-----YSGNLLQVIMSFPSLT- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPACGGDKPGVRTVYLYPNQTGLPDPLSRHHAF-----CFRGISAVPSP---GEEE 686
                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NFLTEVLAYSNSS-----ARGRAFLEHLTDLSIRGTLFVPQNSGLGENE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteoglycan link protein precursor - pig
N'Alternate names: cartilage link protein
C.Species: Sus scrofa domestica (domestic pig)
C.Species: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 22-Jun-1999
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--VFHLRSPLGQYKLTFDKAREACANEAATMATYNQLSYXQKA
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F;274-350/Domain: link protein repeat homology <LNK2>
F;21,56/Binding site: carbohydrate (Asn) (covalent) #status predicted F;61-139/Disulfide bonds: #status predicted
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29.5%; Pred. No. 4.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 --SGVVGIVDYGPRPNKSEMWDVFCY 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 GRYKCE----VIEGL-
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